

## SEQUENCE LISTING

- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
<141> 2000-09-18
- <150> PCT/US00/04414  
<151> 2000-02-22
- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
<151> 1999-07-26
- <150> US 60/146,222  
<151> 1999-07-28
- <150> PCT/US99/20594  
<151> 1999-09-08
- <150> PCT/US99/20944  
<151> 1999-09-13

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20  
<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1  
<211> 1825  
<212> DNA  
<213> Homo sapiens

<400> 1  
actgcacctc gggtctatcg attgaattcc cgggggatcc tctagagatc cctcgacctc 60  
gaccacgcgc tccgggcccgc agcagcacgc cgcaggacc tggagctccg gctgcgtctt 120  
cccgcagcgc taccgcgccat gcgcctgccg cgcggggccg cgctggggct cctgcgcgtt 180  
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgccctg ccaccggtgc 240  
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300  
ggcgggaaca cggcttgagg ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360  
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420  
gaggcgcagg aggagcacct ggaggcctgg tggtgcagc tgaagagcga atatcctgac 480  
ttattcgagt gggtttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540  
cccgaactgtc tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600  
agcggagatg ggagcagaca gggcgacggg tcctgcccgt gccacatggg gtaccagggc 660

```

ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gacccacagc 720
atctgcacag cctgtgacga gtccctgcaag acgtgctcgg gcctgaccaa cagagactgc 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgctt gtgtggatgt ggacgagtgt 840
gcggccgagc cgcctccctg cagcgctgcg cagttctgta agaacgcaa cggctcctac 900
acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc aggaaactgt 960
aaagagtgtg tctctggcta cgcgaggag caccgacagt gtgcagatgt ggacgagtgc 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccaggagagc 1080
tacgtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgccggca 1140
gaggctgaag ccacagaagg agaaagccc acacagctgc cctcccgcga agacctgtaa 1200
tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcctgcagtg gacagcggcg gggagaggct gcctgctctc taacggttga 1320
ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380
ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440
aaaaaaaaaa aaagggcggc cgcgactcta gactcgacct gcagaagctt ggccgccatg 1500
gccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaagt cccaggctc cccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaaccca gtttt 1825

```

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1             5             10             15

```

```

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
      20             25             30

```

```

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35             40             45

```

```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50             55             60

```

```

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65             70             75             80

```

```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85             90             95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100            105            110

```

```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115            120            125

```

```

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130            135            140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300  
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320  
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
 325 330 335  
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
 340 345 350  
 Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

cagggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatacctc tagagatccc 60  
 tcgacctcga cccacgcgctc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120  
 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
 ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gaggcagcatg gcccgaggga 240



ggcgccttccc tgccgcgcgcg ctctggctct ggagcctcct cctgtgcctg ctggcactgc 300  
 gggcggaggc cgggcccgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360  
 caagagtact cataggattt gaagaagata tcctgattgt ttcagagggg aaaatggcac 420  
 cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480  
 attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540  
 ccttgcgctc cctggataaa ggcacatgg cagatccaac cgtcaatgtc cctctgctgg 600  
 gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt ggaaaacagg 660  
 atggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720  
 tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780  
 ggtgccgaaa tggaggcttt tgtaatgaaa gacgcctctg cgagtgtcct gatgggttcc 840  
 acggacctca ctgtgagaaa gccctttgtt cccacgatg tatgaatggt ggactttgtg 900  
 tgactcctgg tttctgcac tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960  
 actgctcaac cacctgcttt aatggaggga cctgtttcta ccctggaaaa tgtatttgcc 1020  
 ctccaggact agaggagag cagtgtgaaa tcagcaaatg cccacaaccc tgtcgaaatg 1080  
 gaggtaaatg cattggtaaa agcaaagtga agtgttccaa aggttaccag ggagacctct 1140  
 gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaaccaaca 1200  
 aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtag gaagccagcc 1260  
 tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgcct tcacttaaaa 1320  
 aggccgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380  
 aaacgtttta agttacacca agttcatagc ctttgttaac ctttcatgtg ttgaatgttc 1440  
 aaataatgtt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500  
 actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatgta 1560  
 tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcaggtta 1620  
 aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tgggtgctgg 1680  
 gggcagggga acatcagaaa gggttaaattg ggcaaaaatg cgtaagtcac aagaatttg 1740  
 atgggtcagt taatgttgaa gttacagcat ttcagatattt attgtcagat atttagatgt 1800  
 ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860  
 ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttacactgtg gtagtggcat 1920  
 ttaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980  
 gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040  
 ttttatactg tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgggcgc gactctagag tcgacctgca 2160  
 gaagcttggc cgccatggcc caacttggtt attgcagctt ataatg 2206

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
 1 5 10 15

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln  
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65					70					75				80	
Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr	Trp	Gln	Ala	Ala	Gly	Gln
				85					90					95	
Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
			100					105					110		
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
		115					120					125			
His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
	130					135					140				
Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu
145					150					155					160
Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
			165					170						175	
Cys	Gln	Gln	Ala	Glu	Cys	Pro	Gly	Gly	Cys	Arg	Asn	Gly	Gly	Phe	Cys
			180					185					190		
Asn	Glu	Arg	Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro	His
		195					200					205			
Cys	Glu	Lys	Ala	Leu	Cys	Thr	Pro	Arg	Cys	Met	Asn	Gly	Gly	Leu	Cys
	210					215					220				
Val	Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val	Asn
225					230					235					240
Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr	Cys
			245						250					255	
Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Glu	Gln
		260					265						270		
Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys	Cys
	275						280					285			
Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr	Gln	Gly	Asp	Leu
	290					295					300				
Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr	Cys
305					310					315					320
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His
			325						330					335	
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala
			340					345					350		

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 5

agggagcacg gacagtgtgc agatgtggac gactgctcac tagca

45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 7

taagtccggc acattacagg tc

22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcatc

49

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9  
 aaagacgcat ctgcgagtgt cc 22

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 10  
 tgctgatttc aactgctct ccc 23

<210> 11  
 <211> 2197  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60  
 ggcccagcc cacaccttca ccagggccca ggagccacca tgtggcgatg tccactgggg 120  
 ctactgctgt tgctgccgct ggctggccac ttggctctgg gtgccagca gggctcgtggg 180  
 cgccgggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccgggtac 240  
 tgccaggagc aggacctgtg ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300  
 ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360  
 ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420  
 ggaggtcgtg tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480  
 caggagaaca ggcagtggca tgggtggatc agacatgatc aaagccatca accagggcaa 540  
 ctatggctgg caggctggga accacagcgc cttctggggc atgaccctgg atgagggcat 600  
 tcgctaccgc ctgggcacca tccgcccatc ttctcggtc atgaacatgc atgaaattta 660  
 tacagtgtctg aaccacagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720  
 caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780  
 agcagctgtg gcatccgacg gtgtctcaat ccatttctctg ggacacatga cgctgtcct 840  
 gtcgcccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gcggtgggcg 900  
 tctcgatggg gcctggtggg tctgcgtcg ccgaggggtg gtgtctgacc actgctacct 960  
 cttctcgggc cgtgaacgag acgaggctgg ccctgcgcc ccctgtatga tgcacagccg 1020  
 agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080  
 caatgacatc taccagggtc ctctgtctc ccgcctcggc tccaacgaca aggagatcat 1140  
 gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200  
 cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260  
 ccgccggcat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

```

tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggcgagag 1380
gggccacttc cgcacgtgc gcggcgtaa tgagtgcgac atcgagagct tcgtgctggg 1440
cgtctggggc cgcgtgggca tggaggacat gggatcacac tgaggctgcg ggcaccacgc 1500
ggggtccggc ctgggatcca ggctaagggc cggcggaaga ggcccgaatg gggcggtgac 1560
cccagcctcg cccgacagag cccggggcgc aggcgggcgc caggcgcta atcccggcgc 1620
gggttccgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680
ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740
caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
caatacccca cccaatccc gtattctttt tttttttttt ttagacaggg tctgtctccg 1860
ttgcccaggc tggagtgcag tggcccatca gggctcactg taacctccga ctctggggtt 1920
caagtgaccc tcccacctca gcctctcaag tagctgggac tacagggtga ccaccacacc 1980
tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggcgtggtt 2040
cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgtg ggattgcagg 2100
catgagccac tgcaccagc cctgtattct tattcttcag atatttattt ttcttttcac 2160
tgtttttaaaa taaaaccaa gtattgataa aaaaaaa 2197

```

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly
  1              5              10              15

```

```

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
      20              25              30

```

```

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35              40              45

```

```

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50              55              60

```

```

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65              70              75              80

```

```

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85              90              95

```

```

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100             105             110

```

```

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115             120             125

```

```

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130             135             140

```

```

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
      145             150             155             160

```

His Asp Pro Gly

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (33)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (80)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (94)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (144)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (188)  
 <223> a, t, c or g

<400> 13  
 aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcggt gtctcaaatac 60  
 caattctctt gggacacatn acgcctgtcc tttngcccca gaacctgctg tcttgtagacac 120  
 ccaccagcag cagggctgcc gcgntgggcg tctcgatggt gcctggtggt tcttgctgcg 180  
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240  
 ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300  
 tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctcctgtcta 360  
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420  
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480  
 gccagtgagc cttgggaggc cagagagata ccgccggcat gggacccact cag 533

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcgggtatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcactgccc tgctgtgcta 60  
ctcctgcaaa gccaggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120  
gggggagcag tgctggaccg cgcgcacccg cgcagttggc ctccctgaccg tcatcagcaa 180  
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240  
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300  
cgccatcctt gcgctgctcc ctgcaactcg cctgctgctc tggggaccg gccagctata 360  
ggctctgggg ggcccgcgtg cagcccacac tgggtgtggt gcccagggc tctgtgccac 420  
tcctcacaga cctggcccag tgggagcctg tcctgggtcc tgaggcacat cctaacgcaa 480  
gtctgaccat gtatgtctgc acccctgtcc cccaccctga cccctccatg gccctctcca 540  
ggactcccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggcccctcca 600  
accctctctg ctgctgtttc catggcccag cattctccac ccttaacctt gtgctcaggc 660  
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc caggctctgg 720  
ccgtgggtgc ccccgacccc agcaggggac aggcactcag gaggggccag taaaggctga 780  
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840  
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900  
aatggcagcc tgagcacagc gtagggcctt aataaacacc tgttggataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

```

cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgccc acctcactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacggt tggcagccgg gttcgcatca aaggggctga 300
gagtgagaag tacatctgta tgaacaagag gggcaagctc atcggggaag ccagcgggaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttccagaa 420
cgcccggcac gagggctggg tcatggcctt cagcggcag gggcgcccc gccaggcttc 480
ccgcagccgc cagaaccagc gcgaggccca cttcatcaag cgctctacc aaggccagct 540
gcccttcccc aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgccccac 600
ccgcccggacc aagcgcacac ggcggcccca gccctcacg tagtctggga ggcagggggc 660
agcagcccct gggccgcctc cccacccctt tcccttctta atccaaggac tgggctgggg 720
tggcgggagg ggagccagat ccccgaggga ggacctgag ggccgcgaag catccagacc 780
cccagctggg aaggggcagg ccggtgcccc agggggcggt ggcacagtgc ccccttccc 840
gacgggtggc aggccttga gaggaactga gtgtcacct gatctcaggc caccagcttc 900
tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960
agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctcagtctgc 1020
ccccagcccc caaactcctc ctggctagac tgtaggaagg gacttttgtt tgtttgtttg 1080
tttcaggaaa aaagaaagg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
acgaccaggg cctgcacccc acccccaact cccagcccc gaataaaaacc attttcttgc 1200

```

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggctcgg catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240  
 tatttttattt ccgtacttca gaaatgggccc tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgccctct gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttccg ggaggetatt agcctcaaat tgttgttttt gtctaagaat cacctgagca 780  
 gtgtgcctgt tgggcttccct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatata cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttc aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccaggtagcg 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

```

aaggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcatctctca 1260
acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcaggggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgacccccgg cctgcctctc ttcaccccag 1380
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cactgattcct gactgggatg 1500
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca tacaaactca 1620
catgggtgaa aatggggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctgggttaact tagagccccg atccacctat cggatttgtt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctcttatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccttttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggt ggtcttgctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcaactgcat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacgggtg tactatataa 2400
tgggatttaa aaaaagtgtc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaactctt                                     2479

```

&lt;210&gt; 28

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

Met Gly Leu Gln Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
 1                      5                      10                      15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
                20                      25                      30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
                35                      40                      45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
 50                      55                      60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65                      70                      75                      80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                85                      90                      95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
                100                      105                      110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
                115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

<210>	29
<211>	21
<212>	DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttgagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctccccc gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

gaggaagacc	cgggtggctg	cgccctgcc	tcgttcccc	gggcgggg	gctgcagcct	180
tgccctctt	gctcgcttg	aaaatggaaa	agatgctcgc	aggctgcttt	ctgctgatcc	240
tcggacagat	cgtcctcctc	cctgcgcgag	ccaggggagcg	gtcacgtggg	aggtccatct	300
ctagggggcag	acacgctcgg	accacccgc	agacggccct	tctggagagt	tctgtgaga	360
acaagcgggc	agacctggtt	tcatcattg	acagctctcg	cagtgtcaac	acccatgact	420
atgcaaaggt	caaggagttc	atcgtggaca	tcttgcaatt	cttggacatt	ggtcctgatg	480
tcacccgagt	gggcctgctc	caatatggca	gcactgtcaa	gaatgagttc	tccctcaaga	540
ccttcaagag	gaagtccgag	gtggagcgtg	ctgtcaagag	gatgcggcat	ctgtccacgg	600
gcaccatgac	tgggctggcc	atccagtatg	cctgaaacat	cgcattctca	gaagcagagg	660
gggcccggcc	cctgagggag	aatgtgccac	gggtcataat	gatcgtgaca	gatgggagac	720
ctcaggactc	cgtggccgag	gtggctgcta	aggcacggga	cacgggcac	ctaactcttg	780
ccattgggtg	gggcaggta	gacttcaaca	ccttgaagtc	cattgggagt	gagcccatg	840
aggaccatgt	cttcttgtg	gccaatttca	gccagattga	gacgctgacc	tccgtgttcc	900
agaagaagtt	gtgcacggcc	cacatgtgca	gcaccctgga	gcataactgt	gccacttct	960
gcatcaacat	ccctggctca	tacgtctgca	gggtgcaaaca	aggctacatt	ctcaactcgg	1020
atcacacgac	ttgcagaatc	caggatctgt	gtgccatgga	ggaccacaac	tgtgagcagc	1080
tctgtgtgaa	tgtgccgggc	tcttctgtct	gccagtgtca	cagtggctac	gccctggctg	1140
aggatgggaa	gaggtgtgtg	gctgtggact	actgtgcctc	agaaaaccac	ggatgtgaac	1200
atgagtgtgt	aaatgctgat	ggctcctacc	tttgccagtg	ccatgaagga	tttgctctta	1260
accagatga	aaaaacgtgc	acaaggatca	actactgtgc	actgaacaaa	ccgggctgtg	1320
agcatgagt	cgtcaacatg	gaggagagct	actactgccg	ctgccaccgt	ggctacactc	1380
tggaccccaa	tggcaaaacc	tgcagccgag	tggaccactg	tgcacagcag	gaccatggct	1440
gtgagcagct	gtgtctgaac	acggaggatt	ccttctgtctg	ccagtgtctca	gaaggcttcc	1500
tcatcaacga	ggacctcaag	acctgctccc	gggtggattta	ctgctctgtc	agtgaccatg	1560
gttgtgaata	ctctctgtgc	aacatggaca	gatccttttgc	ctgtcagttg	cctgagggac	1620
acgtgtctccg	cagcgatggg	aagacgtgtg	caaaattgga	ctcttctgtct	ctgggggacc	1680
acggtttgtga	acattctgtgt	gtaagcagtg	aagattcgtt	tgtgtgccag	tgctttgaag	1740
gttatatact	ccgtgaagat	ggaaaaacct	gcagaaggaa	agatgtctgc	caagctatag	1800
accatggctg	tgaacacatt	tgtgtgaaca	gtgacgactc	atacacgtgc	gagtgtcttg	1860
agggattccg	gctcgtctgag	gatgggaaac	gctgccgaag	gaaggatgtc	tgcaaatcaa	1920
cccaccatgg	ctgcgaacac	atttgtgtta	ataatgggaa	tccctacatc	tgcaaatgct	1980
cagagggatt	tgttctagct	gaggacggaa	gacggtgcaa	gaaatgcact	gaaggcccaa	2040
ttgacctggt	ctttgtgatc	gatggatcca	agagtcttgg	agaagagaat	tttgaggctg	2100
tgaagcagtt	tgtcactgga	attatagatt	ccttgacaat	tccccccaaa	gccgctcgag	2160
tggggctgct	ccagtattcc	acacaggctc	acacagagtt	cactctgaga	aacttcaact	2220
cagccaaaga	catgaaaaaa	gccgtggccc	acatgaaata	catgggaaag	ggctctatga	2280
ctgggctggc	cctgaaacac	atggtttgaga	gaagttttac	ccaaggagaa	ggggccaggc	2340
cctttccac	aagggctgcc	agacggacca	ttgtgttcac	cgcaggacgg	gctcaggatg	2400
acgtctccga	gtgggccagt	aaagccaagg	ccaattggtat	cactatgtat	gctgtttggg	2460
taggaaaagc	cattgaggag	gaactacaag	agattgcctc	tgagccca	aacaagcatc	2520
tcttctatgc	cgaagacttc	agcacaatgg	atgagataag	tgaaaaactc	aagaaaggca	2580
tctgtgaagc	tctagaagac	tccgatggaa	gacaggactc	tccagcaggg	gaactgcca	2640
aaacggtcca	acagccaaca	gaatctgagc	cagtcaccat	aaatatccaa	gacctacttt	2700
cctgttctaa	ttttgcagtg	caacacagat	atctgtttga	agaagacaat	cttttacggg	2760
ctacacaaaa	gctttcccat	tcaacaaaac	cttcaggaag	ccctttggaa	gaaaaacacg	2820
atcaatgcaa	atgtgaaaac	cttataatgt	tccagaacct	tgcaaacgaa	gaagtaagaa	2880
aattaacaca	gcgcttagaa	gaaatgacac	agagaatgga	agccctggaa	aatgcgctga	2940
gatacagatg	aagattagaa	atcgcgacac	atgtgtagtc	attgtatcac	ggattacaat	3000
gaacgcagtg	cagagcccca	aagctcaggc	tattgttaaa	tcaataatgt	tgtgaagtaa	3060
aacaatcagt	actgagaaa	ctggtttgcc	acagaaacaa	gacaagaagt	atacataac	3120
ttgtataaat	ttatctagga	aaaaaatcct	tcaagaattct	aagatgaatt	taccaggtga	3180
gaatgaataa	gtatgtcaag	gtattttgta	atatactgtg	gacacaactt	gtcttgcct	3240
catcctgcct	taqtgtgcaa	tctcatttga	ctatacgata	aaqtttgcac	agtcttactt	3300



```

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360
gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420
ttatacaata ttaaaattca ccacttcag                                     3449

```

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

```

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
  1                      5                      10                      15

```

```

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
          20                      25                      30

```

```

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
      35                      40                      45

```

```

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
      50                      55                      60

```

```

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
      65                      70                      75                      80

```

```

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
          85                      90                      95

```

```

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
      100                      105                      110

```

```

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
      115                      120                      125

```

```

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
      130                      135                      140

```

```

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
      145                      150                      155                      160

```

```

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
          165                      170                      175

```

```

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
      180                      185                      190

```

```

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
      195                      200                      205

```

```

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
      210                      215                      220

```

```

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

```

225		230		235		240									
Met	Cys	Ser	Thr	Leu	Glu	His	Asn	Cys	Ala	His	Phe	Cys	Ile	Asn	Ile
				245					250					255	
Pro	Gly	Ser	Tyr	Val	Cys	Arg	Cys	Lys	Gln	Gly	Tyr	Ile	Leu	Asn	Ser
			260					265					270		
Asp	Gln	Thr	Thr	Cys	Arg	Ile	Gln	Asp	Leu	Cys	Ala	Met	Glu	Asp	His
		275					280					285			
Asn	Cys	Glu	Gln	Leu	Cys	Val	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Gln
	290					295					300				
Cys	Tyr	Ser	Gly	Tyr	Ala	Leu	Ala	Glu	Asp	Gly	Lys	Arg	Cys	Val	Ala
305					310					315					320
Val	Asp	Tyr	Cys	Ala	Ser	Glu	Asn	His	Gly	Cys	Glu	His	Glu	Cys	Val
			325						330					335	
Asn	Ala	Asp	Gly	Ser	Tyr	Leu	Cys	Gln	Cys	His	Glu	Gly	Phe	Ala	Leu
		340						345					350		
Asn	Pro	Asp	Glu	Lys	Thr	Cys	Thr	Arg	Ile	Asn	Tyr	Cys	Ala	Leu	Asn
		355					360					365			
Lys	Pro	Gly	Cys	Glu	His	Glu	Cys	Val	Asn	Met	Glu	Glu	Ser	Tyr	Tyr
	370					375					380				
Cys	Arg	Cys	His	Arg	Gly	Tyr	Thr	Leu	Asp	Pro	Asn	Gly	Lys	Thr	Cys
385					390					395					400
Ser	Arg	Val	Asp	His	Cys	Ala	Gln	Gln	Asp	His	Gly	Cys	Glu	Gln	Leu
			405						410					415	
Cys	Leu	Asn	Thr	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Ser	Glu	Gly	Phe
		420						425					430		
Leu	Ile	Asn	Glu	Asp	Leu	Lys	Thr	Cys	Ser	Arg	Val	Asp	Tyr	Cys	Leu
	435						440					445			
Leu	Ser	Asp	His	Gly	Cys	Glu	Tyr	Ser	Cys	Val	Asn	Met	Asp	Arg	Ser
	450					455					460				
Phe	Ala	Cys	Gln	Cys	Pro	Glu	Gly	His	Val	Leu	Arg	Ser	Asp	Gly	Lys
465					470					475					480
Thr	Cys	Ala	Lys	Leu	Asp	Ser	Cys	Ala	Leu	Gly	Asp	His	Gly	Cys	Glu
			485					490						495	
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Phe	Glu
			500					505					510		

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
                             805                            810                            815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
                             820                            825                            830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
                             835                            840                            845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
                             850                            855                            860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
                             865                            870                            875                            880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
                             885                            890                            895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
                             900                            905                            910

Arg Tyr Arg  
                             915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                             oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                             oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37

gcctgtcagt gtcttgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

```

ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgcagcct 60
cggcacctgc aggtccgtgc gtcccgcggc tggcgccctt gactccgtcc cggccaggga 120
gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcttgg 180
ggctgagtgc cctcgcgccc cctcgcggg cccagctgca actgcacttg cccgccaacc 240
ggttgcaggc ggtggaggga ggggaagtgg tgcttcagc gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaag 360
aaaaggagga tcaggtgttg tctacatca atggggtcac aacaagcaaa cctggagtat 420
ccttgggtcta ctccatgccc tcccggaaac tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccctcctgcc 600
gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag tctccaagga 660
gtaagccgcg tgtccaatac cagtgggatc ggcagcttcc atccttcag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacctttcg tcttccatgg 780
ctggagtcta tgtctgcaag gccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagttag cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccctgg 900
ttggactggg gttgctggct gggctggtec tcttgtagca ccgcccgggc aaggccctgg 960
aggagccagc caatgatata aaggaggatg ccattgctcc ccggaccctg cctggccca 1020
agagctcaga cacaatctcc aagaatggga ccttttctc tgtcacctcc gcacgagccc 1080
tccggccacc ccatggccct cccaggcctg gtgcattgac cccacgccc agtctctcca 1140
gccaggccct gccctcacca agactgccc cgacagatgg ggcccaccct caaccaatat 1200
ccccatccc tgggtggggtt tcttctctcg gcttgagccg catgggtgct gtgcctgtga 1260
tggtgctctg ccagagtcaa gctggtctc tggatatgat accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tctataagg gtcacctcta gcacagaggc ctgagtcagt 1380
ggaaagagtc aactcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gcctccacc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactacca agagtgagg gacagagact ccagtcactg agtctcccag gccccttga 1620
tctgtacccc acccctatct aacaccaccc ttggtcccca ctccagctcc ctgtattgat 1680
ataacctgtc aggttggttt ggtaggttt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tgtagttttc atttgcaaat ttaaataaag atacataatg 1800
ttgtatgaa aaa 1813

```

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
 ctgagccgtg ggctgcagtc tcgc 24  
  
 <210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact gcggccaccg ccaatgaaac gctccccgt cctagtgggt tttccactt 60  
 tggtgaattg ttctataact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacia gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
 aattttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactggt gaacaagcta 720  
 cttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
 atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900  
 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaat ttcagttcca atgagctcaa acccaaccac attatatgaa cttgaaaaaa 1080  
 taacatttac attaagtcac cgaaagggtc cagataggta taggagtcta tgtgcatttt 1140  
 ggaattactc acctgatacc atgaatggca gctgggtctt agagggctgt gagctgacat 1200  
 actcaaatga gaccacacc tcatgccgt gtaatcacct gacacatttt gcaattttga 1260  
 tgcctctggt tccttccatt ggtattaaag attataatat tcttacaagg atcactcaac 1320  
 taggaataat tatttctactg atttgtcttg ccatatgcat ttttaccttc tgggtcttca 1380  
 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440  
 ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500  
 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560  
 tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620  
 tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcactaggat 1680  
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttattttgga 1740  
 gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcacat 1800  
 tataaaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860  
 taaggctctg tgcaagagga gccctcgctc tctgttctt tctcggcacc acctggatct 1920  
 ttgggtttct ccatgttgtg cagcatcag ttggttacagc ttacctcttc acagtcagca 1980  
 atgctttcca ggggatgttc atttttttat tctgtgtgtg tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttggtt tggatgttta aggtaaacat 2100  
 agagaatggg ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160

```

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtatttttaa 2220
atcagttttt ctgttttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
ggaaagtaat tggttttctca ggagtgatat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg tcctgaagga aaccactggc ttgatatttc tgtgactcgt 2460
gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg ttttttctgt agactagctg agaaattggt gacataaaat aaagaattga 2640
agaaacacat ttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agacttctgt ttgctaaatc tgtttctttt tctaattatc taaaaaaaaa aaaaagggtt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa

```

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1             5             10             15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20             25             30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35             40             45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50             55             60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65             70             75             80

```

```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85             90             95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
     100             105             110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
     115             120             125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
     130             135             140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
     145             150             155             160

```

```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
     165             170             175

```

```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

180					185					190					
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val
		195					200					205			
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys
	210						215					220			
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe
225							230					235			240
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys
				245					250					255	
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met
			260					265					270		
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala
	275						280					285			
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser
	290						295					300			
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln
305							310					315			320
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile
				325					330					335	
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys
			340					345					350		
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser
		355					360					365			
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp
	370						375					380			
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser
385							390					395			400
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly
				405					410					415	
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln
			420					425					430		
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr
		435					440					445			
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys
	450						455					460			

```

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465                               470                               475                               480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
                               485                               490                               495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
                               500                               505                               510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
                               515                               520                               525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
                               530                               535                               540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545                               550                               555                               560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
                               565                               570                               575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
                               580                               585                               590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
                               595                               600                               605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610                               615                               620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625                               630                               635                               640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
                               645                               650                               655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
                               660                               665                               670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675                               680                               685

Leu Arg
690

```

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (61)

<223> a, t, c or g

<400> 50

```
tggaaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgagct tgcattttta tattataaga 120
gtattgggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acattttacat taagtcacg aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tgggtcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589
```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggctcctcc tcccgcagat ccgaacggcc tgggcgggggt caccgccgct 120

gggacaagaa gccgcgcgct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttgggcac ctaccggtgg ggcccgtaag gcgctactat ataaggctgc 300  
 cggcccgag cgcgcgcgc gtcagagcag gagcgctgcg tccaggatct agggccacga 360  
 ccatcccaac ccggcactca cagccccgca gcgcacccg gtcgccgcc agcctccgc 420  
 acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gccgggtgtgt 480  
 ggtggtccac gtatggatcc tggcgggct ctggctggcc gtggccgggc gccccctgc 540  
 cttctcggac gccggggccc acgtgcaacta cggctggggc gaccccatcc gcctgcggca 600  
 cctgtacacc tccggccccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660  
 cgtcgtggac tgcgcgcggg gccagagcgc gcacagttt ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcggtgca cagcggtgcg tacctctgca tgggcgccga 780  
 cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840  
 ccgcccagat ggctacaatg tgtaccgato cgagaagcac cgcctcccg tctccctgag 900  
 cagtgcctaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatttct 960  
 gcccatgctg cccatggtcc cagaggagcc tgaggacctc agggggcact tggaatctga 1020  
 catgttctct tcgcccctgg agaccgacag catggaccca tttgggcttg tcaccggact 1080  
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140  
 tgctgccagg ggctgtggtg cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200  
 agtccacgtt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260  
 tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaagcctg 1320  
 tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380  
 gctgcactgt ctcagttctg cttgaatacc tccatcgatg gggaactcac ttcctttgga 1440  
 aaaattctta tgtcaagctg aaattctcta atttttctc atcacttccc caggagcagc 1500  
 cagaagacag gcagtagttt taatttcagg aacaggatgat ccactctgta aaacagcagg 1560  
 taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620  
 ccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680  
 ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa tccccctga 1740  
 ggccagttct gtcattggatg ctgtcctgag aataacttgc tgtcccgggtg tcacctgctt 1800  
 ccatctccca gccaccagc cctctgccca cctcacatgc ctccccatgg attggggcct 1860  
 ccaggcccc ccaccttatg tcaacctgca cttcttgttc aaaaatcagg aaaagaaaag 1920  
 atttgaagac cccaagtctt gtcaataact tgcgtgtgtg aagcagcggg ggaagacct 1980  
 gaaccctttc ccagcactt ggttttccaa catgatatt atgagtaatt tattttgata 2040  
 tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100  
 gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 60

atccgcccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 61

gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta

42

 T  
O  
T  
A  
L  
P  
R  
O  
T  
E  
I  
N  
S  
E  
Q  
U  
E  
N  
C  
E  
S



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggcgccctt gggctatcat aaggcctatg gggtttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggaa aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgatttttaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgcy gggaaatatc gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccgca attctgttgg atatcgagg tgcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggcccttggg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctcttccag aagagtaatt ctctcatctaa agccacgaca atgagtgaat atgtgcagt 960  
 gctcacgcct gtaatcccag cactttggaa ggccgaggcg ggccggtcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggagggttc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact gggttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys	Asp	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	Ala	Ile	Leu	
	35					40				45					
Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys
	50				55					60					
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln
	65			70					75						80
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile
			85					90					95		
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser
		100					105					110			
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu
	115					120					125				
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser
	130				135					140					
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly
	145			150					155					160	
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu
		165					170						175		
Glu	Asn	Pro	Arg	Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met
	180					185						190			
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp
	195					200					205				
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg
	210				215					220					
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile
	225			230					235						240
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu
			245					250					255		
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser
		260				265					270				
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn
	275					280					285				
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala
	290				295				300						
Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe								

305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttggtga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
 ggaagaggat acagtcactc tggaagtatt agtgggtcca gcagttcc 48

<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
 gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaaag 60  
 agaaaagaaga ggaagatggt gggcaacatt tatttaacat gctccacagc ccggaccctg 120  
 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
 aaataaatga attactcaat ctctatgac catctataca tactccacct tcaaaaagta 240  
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300  
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtgggttcta 360  
 tggcattcat catttgacaa atgcaagcat cttccttata aatcagctcc tattgaactt 420  
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtag 540

```

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600
ttacacccag atccatttat atggaagcat ctacagtgga ttgtaatgat ttaggtcttt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaatth atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcttttctg 840
tgtacctaga ggaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatatt aatcacaaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtgggt tgatgctctt ccaaatctag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac tttaagcctc ttatcaatct tgcgcacctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
tctcttttta cgataacagg cttattaaag taccatcatgt tgctcttcaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaatc ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440
gattgtctta cattcaccac aatgcatttt tcagactccc caagctggaa tcaactcatgc 1500
tgaacagcaa tgctctcagt gccctgtacc atgggtaccat tgagtctctg ccaaaccctca 1560
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620
tgaacaaaac caacattcga ttcattggagc cagattcact gttttgcgtg gaccacactg 1680
aattccaagg tcagaatggt cggcaagtgc atttcagggg catgatggaa atttgtctcc 1740
ctcttatagc tcctgagagc tttccttcta atctaaatgt agaagctggg agctatgttt 1800
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860
gtcaaaaact cttgcctaata accctgacag acaagttcta tgtccattct gagggaaacac 1920
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgtata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtgga tggatctttt ccacaagata 2040
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaactca gtgttaaatg gacagccttt gtcaagactg 2160
aaaattctca tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280
aaaacagaaa aaaatgtgta aatgtcacca ccaaagggtt gcaccctgat caaaaagagt 2340
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400
gtgtgatatg tcttatcagc tgccctctctc cagaaatgaa ctgtgatggg ggacacagct 2460
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaattctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtataa gcaactgtta 2580
taggtttacc aacaaatatg tcctaaaaaac caccaaggaa acctactcca aaaatgaac 2639

```

&lt;210&gt; 69

&lt;211&gt; 708

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
  1                      5                      10                      15

```

```

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
          20                      25                      30

```

```

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
          35                      40                      45

```

```

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
          50                      55                      60

```

Ala	Arg	Leu	Pro	Ala	Asn	Thr	Gln	Ile	Leu	Leu	Leu	Gln	Thr	Asn	Asn	
65					70					75					80	
Ile	Ala	Lys	Ile	Glu	Tyr	Ser	Thr	Asp	Phe	Pro	Val	Asn	Leu	Thr	Gly	
				85					90					95		
Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val	
			100					105					110			
Lys	Lys	Met	Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu	
		115					120					125				
Thr	Glu	Leu	Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu	
	130					135						140				
Leu	Tyr	Ile	Asn	His	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Pro	Gly	Ala	Phe	
145					150					155					160	
Ile	Gly	Leu	His	Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Arg	Leu	
				165					170					175		
Gln	Met	Ile	Asn	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile	
			180					185					190			
Leu	Met	Ile	Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe	
		195					200					205				
Lys	Pro	Leu	Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu	
	210					215					220					
Thr	Glu	Ile	Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser	
225					230					235					240	
Ile	Ser	Phe	Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala	Leu	
				245					250					255		
Gln	Lys	Val	Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile	
			260					265					270			
Asn	Arg	Ile	Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His	Leu	Lys	Glu	
		275					280					285				
Leu	Gly	Ile	Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala	
	290					295					300					
Val	Asp	Asn	Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro	
305					310					315					320	
Arg	Leu	Ser	Tyr	Ile	His	Pro	Asn	Ala	Phe	Phe	Arg	Leu	Pro	Lys	Leu	
				325					330					335		
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly	

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
	405	410
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
	420	425
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
	435	440
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
	450	455
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
	465	470
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
	485	490
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
	500	505
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
	515	520
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
	530	535
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
	545	550
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
	565	570
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
	580	585
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
	595	600
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
	610	615
		620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
gcccgggact ggcgcaaggt gcccagcaa ggaaagaaat aatgaagaga cacatgtgtt 60  
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120  
ttaccacgct tgttgaggta gatgaggaat gggctcgtga ttatgctgac attccagcat 180  
gaatctggta gacctgtggt taacccgttc cctctccatg tgtctcctcc taciaagttt 240  
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300  
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360  
tcttctcct gaaacagctct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540  
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600  
aattgccaac aacccctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720  
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaac 780  
taccgattat gccatgctgg tcaccatggt tggctgggtc actatgggtga tctcatatgt 840  
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900  
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960  
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020  
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080  
tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140  
caccctttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200  
tagatccatc tcactattta ataatgaaat ttattttttt aatttaaaag caaataaaaag 1260  
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

accgagccga gcggaaccgaa ggcgcgccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtgag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgctgtca ggctcggcca cgggctgccc gcccgcgtgc gaggctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gagggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agtgcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tgagagcccg cgcttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggcgctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcgtt atcctactgg actacatgtt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcactgtcc tgaggtcccg gcacctcaac atcaatgcca 720
tccgggacta ctccctcaag aggtgtgacc gactcaaggt cttggagatc tccactggc 780
cctacttga caccatgaca cccaactgcc tctacggcct caacctgacg tcctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggcgt cggccacctg gtctatctcc 900
gcttctcaa cctctctac aaccccatca gcaccattga ggcctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctggtgg gcgggcagct ggccgtggtg gagccctatg 1020
ccttccggcg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tgaggaatc agtcttccac tcggtgggca acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtggg tgttccggcg ccgctggcgg ctcaacttca 1200
accggcagca gccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgccc aactacttca cctgcgcgcg cggccgcac cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggcccgatg 1380
gcgacccgcc gcccgccatc ctctggctct caccgcgaaa gcacctggtc tcagccaaga 1440
gcaatgggcg gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gccagggtac 1500
aggacaacgg cacgtacctg tgcctgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactgcgcc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag aggccaacag caccgcgcgc actgtgcctt 1680
tccccttga catcaagacc ctcatcatcg ccaccaccat gggcttcac tcttctctgg 1740
gcgtcgtcct cttctgctg gtgctgtgt ttctctggag ccggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgccc gaaagtccga cgcaggcatc agctccgcg 1860
acgcgcccc caagttcaac atgaagatga tatgagccg gggcgggggg cagggacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgccacctgc tcaactctca gtccctccca 1980
cctcctccct acccttctac acacgttctc tttctccctc ccgcctccgt cccctgctgc 2040
cccccgccag ccctcaccac ctgccctcct tctaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaaa 2290

```

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
                   20                  25                  30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
                   35                  40                  45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
                   50                  55                  60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
                   65                  70                  75                  80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
                   85                  90                  95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
                   100                  105                  110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
                   115                  120                  125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
                   130                  135                  140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
                   145                  150                  155                  160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
                   165                  170                  175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
                   180                  185                  190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
                   195                  200                  205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
                   210                  215                  220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
                   225                  230                  235                  240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
                   245                  250                  255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
                   260                  265                  270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
                   275                  280                  285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
                   290                  295                  300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

	580		585		590										
Ile	Glu	Ile	Glu	Tyr	Val	Pro	Arg	Lys	Ser	Asp	Ala	Gly	Ile	Ser	Ser
	595						600					605			
Ala	Asp	Ala	Pro	Arg	Lys	Phe	Asn	Met	Lys	Met	Ile				
	610						615				620				

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 75

ataccagcta taaccaggct gcg

23

&lt;210&gt; 76

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
gg

50

52

&lt;210&gt; 77

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 gggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
 cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
 aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgc ctttcgggtca 60  
 acatcgtagt ccacccccctc cccatcccca gcccccgagg attcaggctc gccagcgccc 120  
 agccagggag ccggccggga agcgcgatgg gggccccagc cgcctcgtc ctgctcctgc 180  
 tcctgctgtt cgcctgctgc tgggcgccc gcggggcca cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tcctgcaat ggtctaacc tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtag acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt cctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtacgtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggg gaccaagaac 660  
 tccacggaga accaaccgac atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gtcgggtgac attccagggt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttataca 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctggtgc 900  
 tacactgtga gggtcgcggc aatccagtc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgccctgat ctccctttc ctcaacaaga 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgtaaatgac ccagtcctgg tgccctctc ctccagcacc taccacgcca 1140  
 tcacgggtgg gatcgtggct ttcatgtct tctgctgct catcatgctc atcttctctg 1200  
 gccactactt gatccggcac aaaggaaact acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320  
 acaagaagga atatttcac tagaggcgcc tgcccacttc ctgcgcccc cagggggcct 1380  
 gtggggactg ctggggccgt caccaaccgg gacttgtaga gagcaaccgc agggccgccc 1440  
 ctcccgtctg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgctgg 1500  
 tttgtactcg gtttggaatg gggagggagg agggcggggg gaggggaggg ttgccctcag 1560  
 ccctttccgt ggcttctctg catttgggtt attattattt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggtctggaga ggcaggagcc ctgggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

<400> 87  
cctagcacag tgacgaggga cttggc 26

<210> 88  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 88  
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 89  
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
<211> 2755  
<212> DNA  
<213> Homo sapiens

<400> 90  
gggggttagg gaggaaggaa tccaccccca ccccccaaaa cccttttctt ctcttttctt 60  
ggcttcggac attggagcac taaatgaact tgaattgtgt ctgtggcgag caggatggtc 120  
gctgttactt tgtgatgaga tcggggatga attgctcgtt ttaaaaatgc tgctttggat 180  
tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240  
agagaagatc tgttcctgca atgagataga aggggacctc cacgtagact gtgaaaaaaa 300  
gggcttcaca agtctgcagc gtttcactgc cccgacttcc cagttttacc atttatttct 360  
gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggt 420  
tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccgggggctt ttctggggct 480  
gcagctggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540  
ttttctgggg ctggacgatc tggaaatatc ccaggtgat ttttaatttat tacgagatat 600  
agaccggggg gccttccagg acttgaacaa gctggagggtg ctcattttaa atgacaatct 660  
catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tcgacctccg 720  
gggtaacagg ctgaaaacgc tgccctatga ggaggctctg gagcaaatcc ctggtattgc 780  
ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgctct ccctgaaaga 840  
atggctggaa aacattccca agaatgccct gatcggccga gtggtctgcg aagccccac 900  
cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960  
ccgagtggat tctagtctcc cggcgcccc tgcccaagaa gagacctttg ctctggacc 1020  
cctgccaaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

```

aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140
agcgacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200
cagctgcgac cacatcccag ggtcgggttt aaagatgaac tgcaacaaca ggaacgtgag 1260
cagcttggct gatttgaagc ccaagctctc taacgtgcag gagcttttcc tacgagataa 1320
caagatccac agcatccgaa aatcgcaact tgtggattac aagaacctca ttctgttgga 1380
tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440
caggtggcta tacatggata gcaattacct ggacacgtg tcccgggaga aattcgcggg 1500
gctgcaaaac ctagagtacc tgaacgtgga gtacaacgt atccagctca tcctcccggg 1560
cactttcaat gccatgcccc aactgaggat cctcattctc aacaacaacc tgctgaggtc 1620
cctgcctgtg gacgtgttcg ctgggggtctc gctctctaaa ctcagcctgc acaacaatta 1680
cttcatgtac ctcccgggtg caggggtgct ggaccagtta acctccatca tccagataga 1740
cctccacgga aacccctggg agtgcctcct cacaattgtg cttttcaagc agtgggcaga 1800
acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgccgg tgaacttctt 1860
tagaaaggat ttcattgctc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920
ctcgcgccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga cggggacgca 1980
ctccaactcc tacctagaca ccagcagggg gtccatctcg gtgttggtcc cgggactgct 2040
gctggtgttt gtcacctccg ccttcaccgt ggtgggcatg ctctgtttta tcctgaggaa 2100
ccgaaagcgg tccaagagac gagatgcca ctcctccgcg tccgagatta attccctaca 2160
gacagtctgt gactcttcct actggcaca tgggccttac aacgcagatg gggcccacag 2220
agtgtatgac tgtggctctc actcgctctc agactaagac cccaaccca ataggggagg 2280
gcagagggaa ggcgatacat ccttcccac cgcaggcacc cggggggctg gaggggcgtg 2340
taccxaaatc cccgcgccat cagcctggat gggcataagt agataaataa ctgtgagctc 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tgagagagct ggagagcgca gccagctcgc tctttgctga gagcccttt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgcccctgc cctcgcccc ggggcctgtg 2580
gggttggtat ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640
atatctatct ttcctctgtg gattagcccc gtgatggctc cctggttggt acgcagggat 2700
gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

```

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

```

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1              5              10              15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
      20              25              30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
      35              40              45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
      50              55              60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
      65              70              75              80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85              90              95

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttgatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgatgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95  
agtgcactgc gtcccctgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60  
gctgcaccgg gcttggcage gctccgcaca catttctgt cgcggcctaa gggaaactgt 120  
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
 ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300  
 ggggcctcag agaattgaggc cggcggttcgc cctgtgcctc ctctggcagg cgctctggcc 360  
 cgggcctgggc ggccggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420  
 ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcattct 480  
 gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540  
 cctgcgggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600  
 ggagcgcagg cgttccact gcaccctgga gaacgagcct ttgcgggggt tctcctggct 660  
 gtctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720  
 ctctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggtcg agcccgagg 780  
 ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840  
 ggtcttgtgt cctgcgcgcg gcccgggggc cgcctctaac ttgagctatc gcgcgccctt 900  
 ccagctgcac agcgccgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960  
 ccggggacag ctcccgatct cagttacttg catcgcgagc gaaatcggcg ctgcgtggga 1020  
 caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctcgtg ctggcaaagt 1080  
 cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140  
 ctctgagctg ggggaaggac gccgctcttg tgtgaccagt ggggaaggac agccgacct 1200  
 tggggggacc ggggtgccc cccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260  
 gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320  
 agacaattca gtaacatcta ttctcgagat tctctgatgg ggatcacaga gcacgatgtc 1380  
 tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccatc cagggagcgt 1440  
 gatttccaag tttaattcta cgacttcctc tgccactcct caggctttcg actcctcctc 1500  
 tgccgtggtc ttcatatttg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560  
 agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttccagc caaggaagga 1620  
 gtctatgggc ccgcccgggc tggagagtga tcttgagccc gctgctttgg gctccagttc 1680  
 tgcacattgc acaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740  
 ggggtgcctg ctggcggagt cccctcttg ctctagtgat gcatagggaa acaggggaca 1800  
 tgggcactcc tgtgaacagt ttttacttt tgatgaaacg gggaaccaag aggaacttac 1860  
 ttgtgtaact gacaatttct gcagaaatcc cccttctct aaattccctt tactccactg 1920  
 aggagctaaa tcagaactgc aactccttc cctgatgata gaggaagtgg aagtgccttt 1980  
 aggatggtga tactggggga ccgggtagt ctggggagag atattttctt atgtttattc 2040  
 ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100  
 aatttacatt aaaaaataat ttctacaaa atggaaagga aatgttctat gttgttcagg 2160  
 ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220  
 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

```
<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

```
<400> 98
tgaccagtgg ggaaggacag 20
```



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 99  
 acagagcaga gggcgccttg 20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 100  
 tcagggacaa gtggtgtctc tccc 24

<210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 101  
 tcagggaagg agtgtgcagt tctg 24

<210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 102  
 acagctccccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

<210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaaagt cctccgccct gccggccgcg 120
tatcccccg ctaacctgggc cgccccgcgg cggtgcgcgc gtgagaggga gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtctgt gccagtgtga gcggcggtgt gagcgcgggtg 240
ggtgcggagg ggcgtgtgtg ccggcgcgcg ccactctgcc tgctgctggc tgccgccacc 300
gctgccatga ggggcgcgaa cgcctgggcg cactctgcc tgctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gattttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaac cagctggcaa tgggtctcatg 720
gccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
gacagacctt ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttggt tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaattggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtc acctgcgcca 1020
attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag tttactgca 1080
gatgggttta ttggtcacta catattcagg ccaaaaaaac tgcttacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaattttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg togtctgcaa gcagtgcctt ctctcagaa gaggtctaaa ttacattatt 1440
atggggcaag taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca tttaaagetgt attctgccat tgcttttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttgga gcgtttattt atacatctct gtaaaaaggat 1860
atttttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1             5             10             15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
  20             25             30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
  35             40             45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
  50             55             60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360				365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370					375					380				
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390					395					400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
				405					410					415	

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggg tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgcttgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtggcac 420
cgcttctgtg agctgagtga ggagctgggt gagagctggg ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgtct ccccgaggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cggtggttac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc cctgttgccc gatgtcagg acctgaggaa 780
tcaaactgtt tgcaatgcaa gaagggtggt gccctgcata acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaaag gctgcctag gctgcatggg ggcaggggcca 960
ggtcgctgta agaagtgtag ccctggctat cagcagggtg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcatctgtgc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcaactggcca cgctggctgc taaggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcgggcca tgactggcta ctggttgtca 1320
gagcgcagtg accgtgtgct ggagggtctt atcaagggca gataatcgcg gccaccacct 1380
gtaggacctc ctcccaccca cgctgcccccc agagcttggg ctgccctcct gctggacact 1440
caggacagct tggtttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gcccaggtac ccaggcccg gcagacaagg cccctggggg aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttctt taatggtggc tgctagagct ttggcccttg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tctgttctg 1740
tgttcaccac atccccacac cccattggcca cttatttatt catctcagga aataaagaaa 1800
ggtcttggaag agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

```

Arg 65	Asp	Asn	Phe	Gly	Gly 70	Gly	Asn	Thr	Ala	Trp 75	Glu	Glu	Glu	Asn	Leu 80
Ser	Lys	Tyr	Lys	Asp 85	Ser	Glu	Thr	Arg	Leu 90	Val	Glu	Val	Leu	Glu	Gly
Val	Cys	Ser	Lys 100	Ser	Asp	Phe	Glu	Cys 105	His	Arg	Leu	Leu	Glu	Leu	Ser
Glu	Glu	Leu 115	Val	Glu	Ser	Trp	Trp 120	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro
Asp	Leu 130	Phe	Gln	Trp	Leu	Cys 135	Ser	Asp	Ser	Leu	Lys 140	Leu	Cys	Cys	Pro
Ala 145	Gly	Thr	Phe	Gly	Pro 150	Ser	Cys	Leu	Pro	Cys 155	Pro	Gly	Gly	Thr	Glu 160
Arg	Pro	Cys	Gly	Gly 165	Tyr	Gly	Gln	Cys 170	Glu	Gly	Glu	Gly	Thr	Arg	Gly
Gly	Ser	Gly	His 180	Cys	Asp	Cys	Gln	Ala 185	Gly	Tyr	Gly	Gly	Glu	Ala	Cys
Gly	Gln	Cys 195	Gly	Leu	Gly	Tyr	Phe 200	Glu	Ala	Glu	Arg	Asn 205	Ala	Ser	His
Leu 210	Val	Cys	Ser	Ala	Cys	Phe 215	Gly	Pro	Cys	Ala	Arg 220	Cys	Ser	Gly	Pro
Glu 225	Glu	Ser	Asn	Cys	Leu 230	Gln	Cys	Lys	Lys	Gly 235	Trp	Ala	Leu	His	His 240
Leu	Lys	Cys	Val	Asp 245	Ile	Asp	Glu	Cys	Gly 250	Thr	Glu	Gly	Ala	Asn 255	Cys
Gly	Ala	Asp	Gln 260	Phe	Cys	Val	Asn	Thr 265	Glu	Gly	Ser	Tyr	Glu	Cys	Arg
Asp	Cys	Ala 275	Lys	Ala	Cys	Leu	Gly 280	Cys	Met	Gly	Ala	Gly 285	Pro	Gly	Arg
Cys	Lys 290	Lys	Cys	Ser	Pro	Gly 295	Tyr	Gln	Gln	Val	Gly 300	Ser	Lys	Cys	Leu
Asp 305	Val	Asp	Glu	Cys	Glu 310	Thr	Glu	Val	Cys	Pro 315	Gly	Glu	Asn	Lys	Gln 320
Cys	Glu	Asn	Thr 325	Glu	Gly	Gly	Tyr	Arg	Cys 330	Ile	Cys	Ala	Glu	Gly	Tyr 335
Lys	Gln	Met	Glu 340	Gly	Ile	Cys	Val	Lys 345	Glu	Gln	Ile	Pro	Glu	Ser	Ala 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
                   355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
           370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
   385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgccctcttgc tccctccaggg 60  
 cagcaccatg cagccccctgt ggctctgctg ggcaactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatcccca cccacgtgag 240  
 ggcccagtag gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcatggagc agcggctgcc gcccaacagc gagctggtgc aggccgtgct 420  
 gcggtcttcc caggagccgg tccccaaagg cgcgctgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggcctga acttctggca gcagctgagc cggccccggc agccgctgct 660  
 gctacagggtg tcggtgcaga gggagcatct gggcccgtg gcgtccggcg cccacaagct 720  
 ggtccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gacctgaag caccaatgac 840  
 cgagggcacc cgtctgtgcc gccaggagat gtacattgac ctgcagggga tgaagtggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gagggccttg ccttcaagtg gccgtttctg gggcctcgac agtgcctgc 1020  
 ctccgagact gactcgtgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccagggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140  
 gtcctgcca aggaggtcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgaggggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagtgagec ctgaatttgc ttcctctgac aagttacctc 1320  
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
 ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtcctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45



Glu	Glu	Leu	Val	Ile	Pro	Thr	His	Val	Arg	Ala	Gln	Tyr	Val	Ala	Leu
50						55					60				
Leu	Gln	Arg	Ser	His	Gly	Asp	Arg	Ser	Arg	Gly	Lys	Arg	Phe	Ser	Gln
65					70					75					80
Ser	Phe	Arg	Glu	Val	Ala	Gly	Arg	Phe	Leu	Ala	Leu	Glu	Ala	Ser	Thr
				85					90					95	
His	Leu	Leu	Val	Phe	Gly	Met	Glu	Gln	Arg	Leu	Pro	Pro	Asn	Ser	Glu
			100					105					110		
Leu	Val	Gln	Ala	Val	Leu	Arg	Leu	Phe	Gln	Glu	Pro	Val	Pro	Lys	Ala
		115					120					125			
Ala	Leu	His	Arg	His	Gly	Arg	Leu	Ser	Pro	Arg	Ser	Ala	Arg	Ala	Arg
		130				135						140			
Val	Thr	Val	Glu	Trp	Leu	Arg	Val	Arg	Asp	Asp	Gly	Ser	Asn	Arg	Thr
145					150					155					160
Ser	Leu	Ile	Asp	Ser	Arg	Leu	Val	Ser	Val	His	Glu	Ser	Gly	Trp	Lys
				165					170					175	
Ala	Phe	Asp	Val	Thr	Glu	Ala	Val	Asn	Phe	Trp	Gln	Gln	Leu	Ser	Arg
			180					185					190		
Pro	Arg	Gln	Pro	Leu	Leu	Leu	Gln	Val	Ser	Val	Gln	Arg	Glu	His	Leu
		195					200					205			
Gly	Pro	Leu	Ala	Ser	Gly	Ala	His	Lys	Leu	Val	Arg	Phe	Ala	Ser	Gln
	210					215					220				
Gly	Ala	Pro	Ala	Gly	Leu	Gly	Glu	Pro	Gln	Leu	Glu	Leu	His	Thr	Leu
225					230					235					240
Asp	Leu	Gly	Asp	Tyr	Gly	Ala	Gln	Gly	Asp	Cys	Asp	Pro	Glu	Ala	Pro
				245					250					255	
Met	Thr	Glu	Gly	Thr	Arg	Cys	Cys	Arg	Gln	Glu	Met	Tyr	Ile	Asp	Leu
			260					265					270		
Gln	Gly	Met	Lys	Trp	Ala	Glu	Asn	Trp	Val	Leu	Glu	Pro	Pro	Gly	Phe
		275					280					285			
Leu	Ala	Tyr	Glu	Cys	Val	Gly	Thr	Cys	Arg	Gln	Pro	Pro	Glu	Ala	Leu
						295					300				
Ala	Phe	Lys	Trp	Pro	Phe	Leu	Gly	Pro	Arg	Gln	Cys	Ile	Ala	Ser	Glu
305					310					315					320
Thr	Asp	Ser	Leu	Pro	Met	Ile	Val	Ser	Ile	Lys	Glu	Gly	Gly	Arg	Thr
				325					330					335	

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                                  345                                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
                   355                                  360                                  365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 115

aggactgccca taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaa 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acatttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgat cctacgaatc caaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tggcttttga tccccgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaatgctg tgcgcagtga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780
cttghtaacc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtgcccgaa gtgaaggaga attcaaacag acctcgatc tcctgggtgt agcctggctg 960
gctcaccgcc tatcatctgc atttgcctta ctcaggtgct accggactct ggccccctgat 1020
gtctgtagtt tcacaggatg ccttattttg cttctacacc ccacagggcc cctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
tttctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttgggtgt gacactgggg 1440
tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttggt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattttaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaacc tactggaaat acaaagttag ccaggcatgg tggatcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaaa aaaaaaa 1857

```

&lt;210&gt; 119

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1             5             10             15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20             25             30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35             40             45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50             55             60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65             70             75             80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85             90             95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagtg ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg gcgcaggttg 60  
 gagcgtggcg aacaggggct ctgggcctgg cgtgctgct gctgctcggc ctgggactag 120  
 gcctggaggc cggcgccgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
 gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
 tcacctggcg ctgcgcacag gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
 ggattgagcc atgtacccag aaagggcaat gccaccgcgc ccctggcctc ccctgccccct 360  
 gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
 tggcctgcct agcaggcgag ctccgttgca cgtgagcga tgactgcatt ccactcacgt 480  
 ggcgtgcga cggccaccca gactgtccc actccagcga cgagctcggc tgtggaacca 540  
 atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600  
 tcacctctct caggaatgcc acaaccatgg gggccctgtg gacctggag agtgtccccct 660  
 ctgtcgggaa tgccacatcc tctctgccg gagaccagtc tggaagccca actgcctatg 720  
 gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctctccttt 780  
 tgtcctggct ccgagcccag gagcgctcc gccactggg gttactggg gccatgaagg 840  
 agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
 ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtacct 960  
 gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020  
 tctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
 agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
 ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
 aagttgcttc 1210

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cggctctcgct cgctcgcgca gcggcggcag cagagggtcgc gcacagatgc 60  
 ggggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccgca 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgacctg tggtttcagc tggcgctgtg ctccggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaaggcgctt acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600  
 atgaaggatt caagatccgg taccgccgacc tacacaatat ggtttcatta tgcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctcctccc ggtggggact gtgatctcct 780  
 atcgtgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggg gagtcacgga gatttcgtct gccaccgcg gccttgtagag cgctacaacc 960  
 acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020  
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatacag 1080  
 agcaaacgtg gccagcacc catgagaccc tcctgaccac gtggaagatt gtggcggttca 1140



```

cggaaccag tgtgctgctg gtgctgctgc tgcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcgctg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccg 1380
tggaacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggtcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtagagggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1             5             10             15

```

```

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

```

```

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
  35             40             45

```

```

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
  50             55             60

```

```

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
  65             70             75             80

```

```

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

```

```

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
  100            105            110

```

```

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
  115            120            125

```

```

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
  130            135            140

```

```

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
  145            150            155            160

```

```

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
      165            170            175

```

```

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

180					185					190					
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
		195					200					205			
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
	210					215					220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu
225					230					235					240
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe
				245					250					255	
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val
			260					265					270		
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr
	275						280					285			
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
	290					295					300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					320
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
				325					330					335	
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
			340					345					350		
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
		355					360					365			
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
		370				375					380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					400
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
				405					410					415	
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
			420					425					430		
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
		435					440					445			
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
		450				455					460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133  
 atctctatc gctgctttcc cgg 23

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc 23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct 50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggtcgctcg gtggcctaga 60  
 gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg ccgcgcagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctctc 240  
 tgagtgcctc ggatttgac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatthagga actgggtatgt ggatgagccg tcctgcgcca 600
gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccccct 660
acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900
ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgta ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacataataa 1320
aaactgaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta tttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgttggt acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga cttatgaga aggtaccttg ccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaataa aaaaa 1815

```

&lt;210&gt; 137

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<210> 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgagg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactgt 240  
 cctgcaccag cggcggttgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg ttctgacacg gggtcggag 360  
 tcctctcaag cgcctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtgggc cgaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaatgtt tgccctggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt ttctggaatc tggagtccac ccgttggttg ctggctgggc ttttccagt 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtagggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgccg ctgccccgca 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccttgggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttataacc ttaagcccag aaaaataacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
          20             25             30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
          35             40             45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
          50             55             60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
          65             70             75             80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
          85             90             95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
          100            105            110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
          115            120            125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
          130            135            140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
          145            150            155            160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
          165            170            175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa cataacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240  
 gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300  
 agctgccagc ggaacccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360  
 ggtcctcatc caatcagtc gttgcacagg aacagaagat acattggctc agtgtgagca 420  
 agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480  
 gagctctttc tccccagtcc cagaggggtg caggctggct gacggccctg ggcattgcaa 540  
 gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
 cctccgggcc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660  
 aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720  
 ctcaggacga gaagcaacce ttcaggattg cccttctggg ccttggggga agaacacctg 780  
 caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840  
 aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900  
 ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960  
 gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020  
 ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080  
 attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140  
 ggtgggcatc atctaactct ttagtgccct catgggatga acactgatct tcttctgcc ttggactggg 1200  
 atttactgtc tacatgactg catgggatga acactgatct tcttctgcc ttggactggg 1260  
 acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320  
 aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380  
 tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaata 1440  
 cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500  
 tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560  
 acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggtctata 1620  
 atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680  
 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
 85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

```

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
acctacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120
gaagggtgaag gccatggact tcatcaacct cacagccatc ctgcccctgc tgttcgggctg 180
cctgggcgctc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
gaatgctgtg gtggtgatca caggcgccac ctcagggtg ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaagggt cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
gtgctttggc tatgtcgaca tacttgtaa caatgctggg atcagctacc gtggtaccat 540
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
ggtgaccgct atcagccccg gctacatcca caccaacctc tctgtaaatg ccctaccgcg 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgect tccttggtg tttatcttcg aactctggt cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgcccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1              5              10              15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20              25              30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35              40              45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50              55              60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65              70              75              80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85              90              95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100             105             110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115             120             125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130             135             140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145             150             155             160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165             170             175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180             185             190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195             200             205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

210                      215                      220  
 Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
 225                      230                      235                      240  
 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
                     245                      250                      255  
 Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
                     260                      265                      270  
 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
                     275                      280                      285  
 Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
                     290                      295                      300  
 Arg Lys Ser Lys Asn Ser  
 305                      310  
 <210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe  
 <400> 154  
 ggtgctaaac tgggtgctctg tggc                      24  
 <210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe  
 <400> 155  
 cagggcaaga tgagcattcc                      20  
 <210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe

<400> 156  
tcatactggtt ccatctcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatatt agtaaataat gctgggtgtag tctatacatc 480  
agatttgttt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaaag catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aacttttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtg 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagttc 1140  
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac ttatttaaaa 1260  
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtgggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gccactctgt ttcttgagag atacctcaca ttcgaatgcc aaacatttct gcacagggaa 1560  
gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val  
 1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
 20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
 50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255



```

<210> 160
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 160
ggtgaaggca gaaattggag atg
23

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 161
atcccatgca tcagcctgtt tacc
24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 162
gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag
48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
tcagqgagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

```

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
 agaagtgttt ccatgccacc taaggagagac tcaggacagc cattatttct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctggccc tttcccagga 300  
 ctgaacatga agagtatatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360  
 ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
 caggggtggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840  
 tatgcagaat tctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900  
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggttga ggcctttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatggt 1020  
 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080  
 tatgtgaaat ttttgtcact cccagagggtg agacaagcca tccacgtggg gaatcagact 1140  
 tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
 ccattggtaa ctgaaatcat gaataattat aagggttctga tctacaatgg ccaactggac 1260  
 atcatcgtgg cagctgcctt gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
 caggaataca agaaggcaga aaaaaaagtt tggaagatct ttaaactctga cagtgaagtg 1380  
 gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
 attttacct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
 aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagagggttt 1560  
 cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
 tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
 ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740  
 ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
 ttttagggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttgga tgccgtgaag 1920  
 gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaat ggatgaagct 1980  
 ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65		70		75		80
Asn Lys Thr Tyr	Asn Ser Asn Leu Phe	Phe Trp Phe Phe	Pro Ala Gln			
	85	90	95			
Ile Gln Pro Glu Asp	Ala Pro Val Val	Leu Trp Leu Gln	Gly Gly Pro			
	100	105	110			
Gly Gly Ser Ser Met	Phe Gly Leu Phe	Val Glu His Gly	Pro Tyr Val			
	115	120	125			
Val Thr Ser Asn Met	Thr Leu Arg Asp	Arg Asp Phe Pro	Trp Thr Thr			
	130	135	140			
Thr Leu Ser Met Leu	Tyr Ile Asp Asn	Pro Val Gly Thr	Gly Phe Ser			
	145	150	155			160
Phe Thr Asp Asp Thr	His Gly Tyr Ala	Val Asn Glu Asp	Asp Val Ala			
	165	170	175			
Arg Asp Leu Tyr Ser	Ala Leu Ile Gln	Phe Phe Gln Ile	Phe Pro Glu			
	180	185	190			
Tyr Lys Asn Asn Asp	Phe Tyr Val Thr	Gly Glu Ser Tyr	Ala Gly Lys			
	195	200	205			
Tyr Val Pro Ala Ile	Ala His Leu Ile	His Ser Leu Asn	Pro Val Arg			
	210	215	220			
Glu Val Lys Ile Asn	Leu Asn Gly Ile	Ala Ile Gly Asp	Gly Tyr Ser			
	225	230	235			240
Asp Pro Glu Ser Ile	Ile Gly Gly Tyr	Ala Glu Phe Leu	Tyr Gln Ile			
	245	250	255			
Gly Leu Leu Asp Glu	Lys Gln Lys Lys	Tyr Phe Gln Lys	Gln Cys His			
	260	265	270			
Glu Cys Ile Glu His	Ile Arg Lys Gln	Asn Trp Phe Glu	Ala Phe Glu			
	275	280	285			
Ile Leu Asp Lys Leu	Leu Asp Gly Asp	Leu Thr Ser Asp	Pro Ser Tyr			
	290	295	300			
Phe Gln Asn Val Thr	Gly Cys Ser Asn	Tyr Tyr Asn Phe	Leu Arg Cys			
	305	310	315			320
Thr Glu Pro Glu Asp	Gln Leu Tyr Tyr	Val Lys Phe Leu	Ser Leu Pro			
	325	330	335			
Glu Val Arg Gln Ala	Ile His Val Gly	Asn Gln Thr Phe	Asn Asp Gly			
	340	345	350			

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctgggtcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggcttt	tccggctccg	gaatggcaca	tgtgggaatc	ccagtcttgt	tggctacaac	60
atthttccct	ttcctaacaa	gttctaacag	ctgtttctaac	agctagtgat	caggggttct	120
tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
tccttgccctc	tctgtggata	acagagcatg	agaaagtga	gagatgcagc	ggagtgaggt	240
gatggaagtc	taaaatagga	aggaattttg	tgtgcaatat	cagactctgg	gagcagttga	300
cctggagagc	ctgggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	aggggaagact	gggtttagtc	ctaatatcaa	420
attgactggc	tgggtgaact	tcaacagcct	tttaacctct	ctgggagatg	aaaacgatgg	480
cttaaggggc	cagaaataga	gatgctttgt	aaaataaaaat	tttaaaaaaa	gcaagtattt	540
tatagcataa	aggctagaga	ccaaaataga	taacaggatt	ccctgaacat	tcctaagagg	600
gagaaagtat	gttaaaaata	gaaaaaccaa	aatgcagaag	gaggagactc	acagagctaa	660
accaggatgg	ggacctggg	tcaggccagc	ctctttgctc	ctcccgga	ttatttttgg	720
tctgaccact	ctgccttggt	ttttgcagaa	tcattgtgag	gccaaccggg	gaagggtggag	780
cagatgagca	cacacaggag	ccgtctcctc	accgccgccc	ctctcagcat	ggaacagagg	840
cagccctggc	cccgggccct	ggaggtggac	agccgctctg	tggtcctgct	ctcagtggtc	900
tgggtgctgc	tggccccccc	agcagccggc	atgcctcagt	tcagcacctt	ccactctgag	960
aatcgtgact	ggaccttcaa	ccacttgacc	gtccaccaag	ggacgggggc	cgtctatgtg	1020
ggggccatca	accgggtcta	taagctgaca	ggcaacctga	ccatccaggt	ggctcataag	1080
acagggccag	aagaggacaa	caagtctcgt	taccgcgccc	tcattcgtga	gcccctgcagc	1140
gaagtgtctc	ccctcaccaa	caatgtcaac	aagctgctca	tcattgacta	ctctgagaac	1200
cgcttgctgg	cctgtgggag	cctctaccag	gggtctgca	agctgctgag	gctggatgac	1260
ctcttcatcc	tgggtggagc	atcccacaag	aaggagcact	acctgtccag	tgtcaacaag	1320
acgggcacca	tgtacgggg	gattgtgcgc	tctgaggggtg	aggatggcaa	gctcttcac	1380
ggcagcgctg	tggatgggaa	gcaggattac	ttcccagacc	tgtccagccg	gaagctgccc	1440
cgagaccctg	agtcctcagc	catgctcgac	tatgagctac	acagcgattt	tgtctcctct	1500
ctcatcaaga	tcccttcaga	caccctggcc	ctgggtctccc	actttgacat	cttctacatc	1560
tacggctttg	ctagtggggg	ctttgtctac	tttctcactg	tccagcccga	gaccctgag	1620
gggtgtggcca	tcaactccgc	tggagacctc	ttctacacct	cacgcatcgt	gcggctctgc	1680

```

aaggatgacc ccaagttcca ctcatacgtg tccctgccct tcggctgcac cccggccggg 1740
gtggaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgctt gcagtctgcg taccagggcg agggcaacct ggagctcaac 1980
tggtgctggg ggaaggacgt ccagtgcacg aaggcgcttg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
gtggtttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220
tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaggtag ctattggtgg 2280
agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggttaaga 2340
aggggttaat tttgtgactt agcttctagc tacttctctc agccatcagt cattgggtat 2400
gtaaggaatg caagcgattt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1              5              10              15

```

```

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30

```

```

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45

```

```

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60

```

```

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65              70              75              80

```

```

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95

```

```

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100              105              110

```

```

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115              120              125

```

```

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130              135              140

```

```

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145              150              155              160

```

```

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165              170              175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctcccgc gcgcggctga gtgcggactg gagggggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctggctccctc 180  
tgccgctccg ccacgcacag ctggggctgc agggccaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactatct ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480  
acatctgcag tgagatggac ctccggggct tgcccagctg gctactccaa gaccctggca 540  
tgaggctgag gacaacttac aagggtctca ccgaagcagt ggacctttat tttgaccacc 600  
tgatgtccag ggtggtgcc ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagaaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tccctgactt agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgacca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac cacccttctc ttcaacgtcc aggggactca gccaagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcaca tatcttggat tctctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggtcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtcag 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttccggtcca tctcaggcat cctctccct ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680  
ggngttccct cccagaaaca cccacattac ctgctttctt cttgggtagc ttgtccatca 1740  
gctccacgcc ttgtgacacc tttctgaagc tggagggtcg ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttggc cgttactgga acattggacc ccagaagacg ctttacctcc 1860  
caggctccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gcctgcatt acagttcacg gaaaccccc accctggcag gaaccagtac attaatgag 1980  
cgggtgcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc 2040  
ctgggtggct ctgcccacc cctcactgca aaagcatctc ctttaagtagc aacctcaggg 2100  
actggggct acagctctgc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160  
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgcg 2220  
aggctgtcgg gctgtctcta ggggtgggagc agctaactc atcgcccagc ctttggccct 2280

```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcctctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggcttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgctga gaaacatgtg acttccccctt tcccttccca ctcgctgctt cccacagggt 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtg 2640
ctctgggtgtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcctg 3060
ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1              5              10              15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20          25          30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
    35          40          45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
    50          55          60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
    65          70          75          80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85          90          95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
    100          105          110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
    115          120          125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
    130          135          140

```



Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
ccctggtgag gggtctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
aaggggagca aagccgggct cggcccagg cccccaggac ctccatctcc caatgttga 180  
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaaccgcca 240  
tggtcccca gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300  
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360  
tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600  
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
 aggtcttgct gcccaagata tatccatggc tttatcacia tgggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960  
 ctgacaacat gacccaaaatc tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020  
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080  
 ctgtgtcagc tgtaacccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
 tgtacatggt ccatggaggt accaactttg gatattggaa tgggtgccgat aagaaggagc 1200  
 gcttccttcc gattactacc agctatgact atgatgcacc tatacttgaa gcaggggacc 1260  
 ccacacctaa gctttttgct cttcgagatg tcacagcaa gttccaggaa gttcctttgg 1320  
 gacctttacc tcccccgagc cccaagatga tgcctggacc tgtgactctg cacctgggtg 1380  
 ggcatttact ggctttccta gacttgcttt gcccccgagg gccattcat tcaatcttgc 1440  
 caatgacctt tgaggctgtc aagcaggacc atggettcat gttgtaccga acctatatga 1500  
 cccataccat ttttgagcca acaccattct ggggtgccaa taatggagtc catgaccgtg 1560  
 cctatgtgat ggtggatggg gtgttccagg gtgttgggga gcgaaatat agagacaaac 1620  
 tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740  
 aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800  
 ggtttcccct ccagttgcca aaatggccat atcctcaagc tccctctggc cccacattct 1860  
 actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920  
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980  
 ggccacaaca gacctctac gtgccaaagat tccctgctgt tccatgggga gccctcaaca 2040  
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100  
 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160  
 atacactgag tgctctgaa ccaatggagt taagtgggca ctgaaaggta ggcggggcat 2220  
 ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280  
 tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
 aaattagccg ggcgtgatgg tgggcacctc taatccagc tacttgggag gctgagggca 2400  
 ggagaattgc ttgaatccag gaggcagagg ttgcagtgag tggaggttgt accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

	340		345		350												
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro		
	355						360					365					
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu		
	370					375					380						
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu		
385					390					395					400		
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr		
				405					410					415			
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val		
			420					425					430				
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val		
	435						440					445					
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr		
	450					455					460						
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg		
465					470					475					480		
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro		
				485					490					495			
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu		
			500					505					510				
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys		
	515						520					525					
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr		
	530					535					540						
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly		
545					550					555					560		
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr		
				565					570					575			
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu		
			580					585					590				
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu		
	595						600					605					
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu		
	610					615					620						

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccacag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtggt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420  
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgccctcacg tgaagttcac tgatgtgggt gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtgggt ccacatctta 840  
 caaagttagt cttcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattctctcc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcatatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaa gggacattct gccaaaacaa ttgttttaaat 1320

```

gcataaaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaattg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta ggggttttaag tcattcattt ccaaatacatt tttttttttc ttttggggaa 1800
agggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgctgtctaa agtaaatgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaaa
1947

```

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85             90             95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
     100             105             110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
     115             120             125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
     130             135             140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
     145             150             155             160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
     165             170             175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
     180             185             190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                                      470                                      475                                      480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro

                                    485                                      490                                      495

Phe Ala Asn Gly Ile

                                    500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                                     oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c                                      21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                                     oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg                                      24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                                     oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag                                      47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcattttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccttggg 120  
 aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctcccttg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
 atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360  
 ttcaaaatac acaacgcgct aaaagctgca aaggaaacctg aagctgtggc tgtaaaaaat 420  
 cacaacccag acaaggtgtg gtgggccaaag aacagccagg ccaaaacccat tgccacggag 480  
 tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
 cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780  
 ggggagagag aaccctcact gtgggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctacacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tgggtcctta aggctgcccc gcgccttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcc a ttgacctct taattctctc ctgtttgccg 1020  
 gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtc aggggggtgcc 1080  
 aatatggcag agaccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttcctgtatt tgaatcatca 1320  
 tccagtcacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
 gtcttctact acttcttctc tctaacatc tctattccaa actgtggcgg ttacctggat 1440  
 accttggaa gaccttccac cagccccaat tacccaaagc cgcctcctga gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
 ttctagaaa tagacaaaca gtgcaaattt gattttcttg ccatctatga tggccctcc 1620  
 accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacctt cgaatcgtca 1680  
 tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
 gcttcctaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800  
 gacaggatga gagttattat aagcaaatcc tactagagg cttttaactc taatgggaat 1860  
 aacttgcaac taaaagaccc aacttgacaga ccaaaattat caaatgttgt ggaattttct 1920  
 gtcctctcta atggatgtgg tacaatcaga aaggtagaag atcagtcatt tacttacacc 1980  
 aatataatca ccttttctgc atcctcaact tctgaagtga tcaccctga gaaacaactc 2040  
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
 gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaaccag catggctctt 2160  
 tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
 caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280  
 gatacctgta gagcctctcc cacctctgac tttgcactc caacctacga cctaatacaag 2340  
 agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
 ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
 gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaagggtg tgtctccaga 2520  
 agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
 ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640  
 gaaactccaa accagccttt caacagtgtg catctgtttt ccttcatggg tctagctctg 2700  
 aatgtggatga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaa ctattaaacta acaggtccaa ccctaagtga gacatgtttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggctgaaaag tgacacacag gcctgcatgt aaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
		580						585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
	595						600					605			

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgcctgcc cacagcgcca cgcgcttcga cccacctgg 180



gagtccctgg acgccccgcca gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240  
 atccactggg gagtggttttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300  
 caaaaaggaaa agataaccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360  
 aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgcca ccagtgggca 420  
 gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480  
 tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggccaag 540  
 agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttgga 600  
 ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660  
 ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720  
 aactatcagc ctgagggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780  
 aacagcacag gcttcttggc ctgggtatat aatgaaagcc cagttcgggg cacagtagtc 840  
 accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900  
 gatcgttata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960  
 aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020  
 ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaatattggg 1080  
 cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtggggctc 1140  
 tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200  
 actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260  
 tttcttaaat ggcccacatc aggcacagctg ttcttggcc atcccaaagc tattctgggg 1320  
 gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380  
 aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440  
 tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500  
 atgtctaagg ctaggaacta tcagggtgtc ataattgtag cacatggaga aagcaatgta 1560  
 aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620  
 ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680  
 cattgatttg tttccatgtg tgactcagag gtgagaatth tttcacatta tagtagcaag 1740  
 gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800  
 tatatagtta tgcacactt aatatgggga tattttctgg gaaatgcatt gctagtcaat 1860  
 ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920  
 cacaccta atgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980  
 actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040  
 gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100  
 gaatggagct tacaggactg gaagtgtgctc tgggtgagtc agtgagtga tgtgaaggcc 2160  
 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220  
 ttataaaaaa agttttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280  
 caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2340  
 taaactcatt gtgcaaatgt aa 2362

&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu  
 1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
 35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
450 455 460

Asn Val Ile  
465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgacagc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcaggga aa tccggatgct tccggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttccctgg ctctgaagggt gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcacttccat ctggaccacg aggtctcctg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccaggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggctatc tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tctcctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctg cagctggtct tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960  
 tttacaaaca agaactcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaaatc aagaaaactg ataaaaaccc agaagagctc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgctcctt acctgcccc agctggggaa 1200  
 atcaaaaggg ccaagaagacc aaagaagaaa gtccaccctt gggtcctaac tgggaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tctatctctc ctacctccaa agcttccac gccctttcta gcctggctat 1380  
 gtcttaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgttttag aacacacaca cttacttttt ctggtctcta ccactgctga tattttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggagctat 2100
ttttttcagt tttgatattt ctagcttctc tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1             5             10             15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20             25             30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35             40             45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50             55             60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65             70             75             80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85             90             95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100            105            110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115            120            125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130            135            140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgcaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcgggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggt aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttcgcatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccac ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
tggagttctt tgccaattgg tctaataact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acaggggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgaaca catcacccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgccggcgcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatagac 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac cccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttcctct cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcacc ctaggaagg cctgccatgc 1080
tgtggccaac tgtttcaact gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttggtt 1260
agacctagat ttaaccctaa ggtaagatgc tgggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttctgg ctctgcttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttgaggga gaaatccctt ggactttcac taaccctctg 1560
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1              5              10              15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65              70              75              80

```



```
<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 208
gcttggatat tcgcatgggc ctac
```

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcctggcccc ggtcacctcg gcatgaggag atgggcctgt tgctcctggg 120  
 cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240  
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgctaccgct acgagccggc cctggctctcc ccgcggcggtg tgcgtgtcaa 360  
 atgggtggaag ctgtcggaga acggggcccc agagaaggac gtgctgggtg ccatcgggct 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtggg 600

```

ctttccttac cagtccccca acggggcgcta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tgggtggcctc ctttgagcag ctcttcggg cctgggagga 720
gggcctggac tgggtgcaacg cgggctgggt gcaggatgct acgggtgcagt accccatcat 780
gttgcctcgg cagccctgcg gtggcccagg cctggcacct ggcgtgcaaa gctacggccc 840
ccgccaccgc cgctgcacc gctatgatgt attctgcttc gctactgcc tcaaggggcg 900
ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960
ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080
cccgcatact aactgtgggc cccagagacc tgggggtccga agctttgggt tccccgacct 1140
gcagagccgc ttgtacggtg tttactgcta ccgccagcac taggacctgg ggcctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tactttotcaa tttaaatttt ctttaaacad ttttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380
aatcatgctt gctcccctgg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440
atccaggctg gtctccctcc cttaaggagg ttggtgcccc gagtgggagg tggcctgtct 1500
agaatgccgc cgggagtcgg ggcaggtggg gcacagttct cctgccccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
cttctctgtg aagccgctga cccagctctg cccactgagg ggctagggtt ggaagccagt 1680
tctaggcttc caggcgaaat ctgagggaag gaagaaactc cctccccgt tccccctccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tctgttttc ctgtgtgggg 1800
aggggccctc aggtgtgtgt actttggaca ataaatgggt ctatgactgc cttccgccaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa                                           1985

```

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

```

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1                      5                      10                      15

```

```

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
          20                      25                      30

```

```

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
          35                      40                      45

```

```

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
          50                      55                      60

```

```

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
          65                      70                      75                      80

```

```

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
          85                      90                      95

```

```

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
          100                      105                      110

```

```

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115					120					125								
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr			
130					135					140								
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu			
145					150					155					160			
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg			
					165					170					175			
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala			
					180					185					190			
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly			
					195					200					205			
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr			
					210					215					220			
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro			
					225					230					235		240	
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp			
					245					250					255			
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu			
					260					265					270			
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu			
					275					280					285			
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys			
					290					295					300			
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser			
					305					310					315		320	
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu			
					325					330					335			
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr			
					340					345					350			
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His											
					355					360								

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttggtg ggttgagg 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtggag gaaatgag 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ggagagcggg gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
 gcttctgttg ctactgaggg acggggccca ggggaagcca tccccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180  
 cgggaaactc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgcgct ggccgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcgcttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg cccccgagg agttccctca catgcgggac atcgtgattg ctgaaacctc 660  
 ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tggggccactg 840  
 ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
 agcaccgcgc acctgccaca gcctcagagg cccgcacaat gaccggagga ggggcccgtg 1080  
 tggctctggc cctccctgt ccaggcccc caggaggcag atgcagtccc aggcacctc 1140  
 ctgcccctgg gctctcaggg accccctggg tcggcttctg tccctgtcac accccaacc 1200  
 ccaggagggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260  
 cagcccagac ccagggacct ttggcccaa gctcagctct aagaaccgcc ccaacccctc 1320  
 cagctccaaa tctgagcctc caccacatag actgaaactc cctggcccc agccctctcc 1380  
 tgccctggcct ggccctggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 ggggccttgc cttccgcact cgggcgcagc cgggtggatc tgcagcaggt ggcggagcccc 60  
 gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgtcgtcggt ttggcgcccc cgcctccccg cgggtgcgggg ttgcacaccg 180  
 atcctgggct tgcgtcgatt tgcgcgcag ggcgcctcca gacctagagg ggcgctggcc 240  
 tggagcagcg ggtcgtctgt gtccctctctc ctctgcgcgc cgcgcgggga tccgaagggg 300  
 gcggggctct gaggagggtga cgcgcggggc ctcccgcacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggctc 420  
 tcggcctcgg tgtgtgtctg ctgctgctgc cggggccccg ggcagcgcag ggagccgctc 480  
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgcccagg gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600  
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cctggtcgag aaaactattc ctcagtagat gccaatggca 720  
 tccagtctca aatgctttct agatggctctg cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
 tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140  
 agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccaag 1200  
 tgggtggtgg atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgttg 1260  
 ccagagagtt tgggtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320  
 tggggatggg tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380  
 tctcttacca catgccaac tggtttggca ccacaaaata cgtaaagcct ctggtacaga 1440  
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500  
 cctttctaata tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560  
 ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620  
 tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680  
 atgtccctagc tgtcatcaga aacatccgct atatgagtgg tggaaacagct actggtgatg 1740  
 ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800  
 tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860  
 cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920  
 tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gatttcacag 1980  
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040  
 agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100  
 attgtattct cataatactg aaatgcttta gcatactaga atcagatata aaactattaa 2160  
 gtatgtcaac agccatttag gcaaataagc actcctttaa agccgctgcc ttctgggttac 2220  
 aatttacagt gtactttgtt aaaaaactg ctgaggcttc ataatacatg ctcttagaaa 2280  
 ctcaggaaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340  
 tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400  
 aaa 2403

<210> 227

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu  
 1 5 10 15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile  
 20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
 65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
 85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
 100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
 115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
 130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
 145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
 165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
 195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
 225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
 245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc 18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc 18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc 18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233

cttggcacca atgtccgaga tttc

24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234

gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

cgccgcgctc ccgcacccgc ggcccgccca ccgcgcgct cccgcatctg caccgcgagc 60  
 ccggcgccct ccggcgccga gcgagcagat ccagtcgggc ccgcagcgca actcggtcca 120  
 gtcggggcgg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gctgctgctt ggccggcgcg gtccccacgg ccccgcgcc cgctccgacg gcgacctcgg 240  
 ctccagtcga gcccggcccg gctctcagct accgcagga ggaggccacc ctcaatgaga 300  
 tgttcgcgga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcag 600  
 acgaggactg tggggccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

```

gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
accagagggg ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840
tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttcttg 900
acctcatcac ctgggagcta gagcctgatg gagccttga cggatgcctt tgtgccagt 960
gcctcctctg ccagccccac agccacagcc tgggtgatgt gtgcaagccg accttcgtgg 1020
ggagccgtga ccaagatggg gagatcctgc tggccagaga ggtccccgat gagtatgaag 1080
ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140
aagagatggc gctgggggag cctgcggctg ccgccgctgc actgctggga ggggaagaga 1200
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt tatttcccca 1260
ggtgtgtgct ttaggcgtgg gctgaccagg cttcttctta catcttcttc ccagtaagtt 1320
tcccctctgg cttgacagca tgaggtgttg tgcatttgtt cagctcccc aggctgttct 1380
ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaactgca ggagcagttt 1440
gccacccttg tccagattat tggctgcttt gcctctacca gttggcagac agcgtttgt 1500
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560
tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaacatc aacctggcaa 1620
aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680
cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740
gtgttgctca gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800
tctctcagca cagcctgggg aggggggtcat tgttctcttc gtccatcagg gatctcagag 1860
gctcagagac tgcaagctgc ttgcccaggt cacacagcta gtgaagacca gagcagtttc 1920
atctggttgt gactctaagc tcagtgtctt ctccactacc ccacaccagc cttggtgcca 1980
ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
attaaggtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160
ctttggcagt tgcattagta actttgaaag gtatatgact ggcgtagca tacagggttaa 2220
cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460
taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaa

```

&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

```

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
  1                      5                      10                      15

```

```

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
                20                      25                      30

```

```

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
        35                      40                      45

```

```

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                      55                      60

```

```

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
    65                      70                      75                      80

```

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                             85                            90                            95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                             100                            105                            110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                             115                            120                            125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                             130                            135                            140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                             145                            150                            155                            160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                             165                            170                            175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                             180                            185                            190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                             195                            200                            205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                             210                            215                            220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                             225                            230                            235                            240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                             245                            250                            255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                             260                            265                            270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                             275                            280                            285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                             290                            295                            300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                             305                            310                            315                            320  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
                             325                            330                            335  
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
                             340                            345                            350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 237  
 ggagctgcac cccttgc 17  
  
 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
 gcagagcgga gatgcagcgg cttg 24  
  
 <210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
 ttggcagctt catggagg 18  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
 cctgggcaaa aatgcaac 18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc 24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacatata 150  
 cacacatata ccttctcttc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250  
 attacctctg cagctccttt ggcttgttga gtcaaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcatthttg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

ggggtagata	ctgcttctct	gcaacctcct	taactctgca	tctcttctt	650
ccagggtctgc	ccctgatggg	gcctggcaat	gactgagcag	gccagcccc	700
agaggacaag	gaagagaagg	catattgagg	agggcaagaa	gtgacgccc	750
gtgtagaatg	actgccctgg	gagggtggtt	ccttgggccc	tggcaggggt	800
gctgaccctt	accctgcaaa	acacaaagag	caggactcca	gactctcctt	850
gtgaatggtc	ccctgccctg	cagctccacc	atgaggcttc	tcgtggcccc	900
actcttgcta	gcttgggtgg	ctggtgccac	tgccactgtg	cccgtggtac	950
cctggcatgt	tccctgcccc	cctcagtgtg	cctgccagat	ccggccctgg	1000
tatacgcccc	gctcgtccta	ccgcgaggct	accactgtgg	actgcaatga	1050
cctattcctg	acggcagtcc	ccccggcact	ccccgcaggc	acacagaccc	1100
tgctcctgca	gagcaacagc	attgtccgtg	tggaccagag	tgagctgggc	1150
tacctggcca	atctcacaga	gctggacctg	tcccagaaca	gcttttcgga	1200
tgcccgagac	tgtgatttcc	atgccttgcc	ccagctgctg	agcctgcacc	1250
tagaggagaa	ccagctgacc	cggctggagg	accacagctt	tgcagggctg	1300
gccagcctac	aggaactcta	tctcaaccac	aaccagctct	accgcatcgc	1350
ccccagggcc	ttttctggcc	tcagcaactt	gctgcggctg	cacctcaact	1400
ccaacctcct	gagggccatt	gacagccgct	ggtttgaaat	gctgcccac	1450
ttggagatac	tcatgattgg	cggcaacaag	gtagatgcca	tcttggacat	1500
gaacttcggg	cccttggcca	acctgcgtag	cctgggtgcta	gcaggcatga	1550
acctgcggga	gatctccgac	tatgccttgg	aggggtgca	aagcctggag	1600
agcctctcct	tctatgacaa	ccagctggcc	cgggtgcccc	ggcgggcact	1650
ggaacaggtg	cccgggctca	agttcctaga	cctcaacaag	aaccgcctcc	1700
agcgggtagg	gccgggggac	tttgccaaca	tgctgcacct	taaggagctg	1750
ggactgaaca	acatggagga	gctggtctcc	atcgacaagt	ttgccttgg	1800
gaacctcccc	gagctgacca	agctggacat	caccaataac	ccacggctgt	1850
ccttcatcca	ccccgcgcc	ttccaccacc	tgccccagat	ggagaccctc	1900
atgctcaaca	acaacgctct	cagtgccttg	caccagcaga	cgggtggagtc	1950



ctccaaggaa caggagggac tttggctaga gcctcctgcc tccccatctt 3300  
 ctctctgccc agaggctcct gggcctggct tggtgtgcc ctacctgtgt 3350  
 ccccggtgtg cacccttcc ttttctttt ctctgtacag tctcagttgc 3400  
 ttgtctttgt gcctcctggg caagggctga aggaggccac tccatctcac 3450  
 ctcggggggc tgcctcaat gtgggagtga cccagccag atctgaagga 3500  
 catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550  
 ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
 atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
 aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly
1				5					10					15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro
				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
				35					40					45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
				50					55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
				110					115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
				140					145					150

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	
				155					160					165	
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	
				170					175					180	
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	
				185					190					195	
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	
				200					205					210	
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	
				215					220					225	
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	
				230					235					240	
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	
				245					250					255	
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	
				260					265					270	
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	
				275					280					285	
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	
				290					295					300	
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	
				305					310					315	
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	
				320					325					330	
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	
				335					340					345	
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	
				350					355					360	
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	
				365					370					375	
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	
				380					385					390	
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	
				395					400					405	
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	

				410					415					420
Leu	Pro	Leu	Ile	Ser 425	Pro	Arg	Ser	Phe	Pro 430	Pro	Ser	Leu	Gln	Val 435
Ala	Ser	Gly	Glu	Ser 440	Met	Val	Leu	His	Cys 445	Arg	Ala	Leu	Ala	Glu 450
Pro	Glu	Pro	Glu	Ile 455	Tyr	Trp	Val	Thr	Pro 460	Ala	Gly	Leu	Arg	Leu 465
Thr	Pro	Ala	His	Ala 470	Gly	Arg	Arg	Tyr	Arg 475	Val	Tyr	Pro	Glu	Gly 480
Thr	Leu	Glu	Leu	Arg 485	Arg	Val	Thr	Ala	Glu 490	Glu	Ala	Gly	Leu	Tyr 495
Thr	Cys	Val	Ala	Gln 500	Asn	Leu	Val	Gly	Ala 505	Asp	Thr	Lys	Thr	Val 510
Ser	Val	Val	Val	Gly 515	Arg	Ala	Leu	Leu	Gln 520	Pro	Gly	Arg	Asp	Glu 525
Gly	Gln	Gly	Leu	Glu 530	Leu	Arg	Val	Gln	Glu 535	Thr	His	Pro	Tyr	His 540
Ile	Leu	Leu	Ser	Trp 545	Val	Thr	Pro	Pro	Asn 550	Thr	Val	Ser	Thr	Asn 555
Leu	Thr	Trp	Ser	Ser 560	Ala	Ser	Ser	Leu	Arg 565	Gly	Gln	Gly	Ala	Thr 570
Ala	Leu	Ala	Arg	Leu 575	Pro	Arg	Gly	Thr	His 580	Ser	Tyr	Asn	Ile	Thr 585
Arg	Leu	Leu	Gln	Ala 590	Thr	Glu	Tyr	Trp	Ala 595	Cys	Leu	Gln	Val	Ala 600
Phe	Ala	Asp	Ala	His 605	Thr	Gln	Leu	Ala	Cys 610	Val	Trp	Ala	Arg	Thr 615
Lys	Glu	Ala	Thr	Ser 620	Cys	His	Arg	Ala	Leu 625	Gly	Asp	Arg	Pro	Gly 630
Leu	Ile	Ala	Ile	Leu 635	Ala	Leu	Ala	Val	Leu 640	Leu	Leu	Ala	Ala	Gly 645
Leu	Ala	Ala	His	Leu 650	Gly	Thr	Gly	Gln	Pro 655	Arg	Lys	Gly	Val	Gly 660
Gly	Arg	Arg	Pro	Leu 665	Pro	Pro	Ala	Trp	Ala 670	Phe	Trp	Gly	Trp	Ser 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                   680                                  685                                  690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                   695                                  700                                  705

Leu Pro Pro Leu Ser Gln Asn Ser  
                   710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag gcgctgtttg agaagggtgaa gaagttccgg acccatgtgg 50

aggaggggga catttgtgtac cgcctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcatectcat catctgtctac accgtctact acgtgcacaa 150

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
accgcaccta ccgctgtgcc caccacctgg ccacactctt caagatcctg 250  
gcgtccttct acatcagcct agtcactctt tacggcctca tctgcatgta 300  
cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350  
cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400  
ttcgctttca tgctgcacct cattgaccaa tacgacctgc tctactcaa 450  
gcgttctgcc gtcttctgt cggaggtgag tgagaacaag ctgcggcagc 500  
tgaacctcaa caacgagtgg acgctggaca agctccggca gcggtcacc 550  
aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600  
ccctgacact gtgtttgacc tgggtggagct ggaggtcctc aagctggagc 650  
tgatccccga cgtgaccatc ccgccagca ttgccagct cacgggcctc 700  
aaggagctgt ggctctacca cacagcggcc aagattgaag cgctgcgct 750  
ggccttctg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800  
tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850  
cacctgacgg gcaacctgag cgcggagaac aaccgctaca tcgtcatcga 900  
cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950  
taagcaagct gccacaggtg gtcacagatg tgggcgtgca cctgcagaag 1000  
ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050  
gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100  
gcatcccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150  
aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200  
gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250  
ccatccagat cggcaacctc accaacctgg agcgcctcta cctgaaccgc 1300  
aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350  
ctacctggac ctcagccaca acaacctgac cttcctccct gccgacatcg 1400  
gcctcctgca gaacctccag aacctagcca tcacggccaa ccggatcgag 1450



[illegible]

aacggtgctc cattgcacc tcccctcctc gtgctgccc tgcctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca ctgcgccag actttgtttc 2900  
 cccacctcct gcggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 ctcccatcag cctgtcgcc acctggctct tcatgaagag cagacactta 3000  
 gaggttggtc gggaaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgctcct ggcgcctgga gtgcacacag cccagtcggc 3100  
 acctggtggc tggaagccaa cctgctttag atcactcggg tccccacctt 3150  
 agaagggtcc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttgtg 3250  
 ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccggt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400  
 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10				15	
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
			20						25				30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40				45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55				60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70				75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

95										100					105				
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro					
				110					115					120					
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu					
				125					130					135					
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp					
				140					145					150					
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu					
				155					160					165					
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp					
				170					175					180					
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val					
				185					190					195					
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu					
				200					205					210					
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala					
				215					220					225					
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp					
				230					235					240					
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu					
				245					250					255					
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr					
				260					265					270					
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu					
				275					280					285					
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp					
				290					295					300					
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr					
				305					310					315					
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr					
				320					325					330					
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser					
				335					340					345					
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn					
				350					355					360					

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

caacaatgag ggcaccaagc 20

&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggt gggttgetget getgccgetg ctgetggggc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggatcatgt 250  
 ggcttcaggg cggccaggc gggtctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtagggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatgggtggc 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca tttctcaga gtcctatgga ggaaaaatgg 550  
 cagctggcat tggcttagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650  
 tgattcgggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
gccgtaaata agggggtcta cagagaggcc acagagctgt gggggaaagc 800  
agaaatgatac attgaacaga acacagatgg ggtgaacttc tataacatct 850  
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
agatgcctta agccagctca tgaatggccc catcagaaaag aagctcaaaa 1000  
ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050  
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
tcgtagatac catgggtcag gaggcctggg tgcggaaaact gaagtggcca 1200  
gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
taaactcttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300  
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600  
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20					25					30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35					40					45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	
				50					55					60	
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	
				65					70					75	
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	
				80					85					90	
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	
				95					100					105	
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	
				110					115					120	
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	
				125					130					135	
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	
				140					145					150	
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	
				155					160					165	
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	
				170					175					180	
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	
				185					190					195	
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	
				200					205					210	
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	
				215					220					225	
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	
				230					235					240	
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	
				245					250					255	
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	
				260					265					270	
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	
				275					280					285	
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	
				290					295					300	
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly	

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

```

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tgagagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgcgcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgccca tccttctgga 350
gcctgcagggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```



cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500  
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600  
 tcaggctgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650  
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700  
 caaggcggga aggatgcctg cttcgggtgac tcagggtggac ccttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtggtcg gcccaatcgg cccggtgtct acaccaatat cagccaccac 850  
 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900  
 cccctcctgg ccactactct ttttcctct tctctgggct ctcccactcc 950  
 tggggccggg ctgagcctac ctgagcccat gcagcctggg gccactgcc 1000  
 agtcaggccc tggttctctt ctgtcttggt tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1				5					10					15

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
				20					25				30	

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
				35					40				45	

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
				50					55				60	

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
				65					70				75	

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
				80					85				90	

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcctcctctc tggcaaatgc agttacagcc 100  
 cggagccccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250  
 ctctcctaata cggaaaatac ctgaccctag agaattgtggc tgatctgggtg 300  
 aggccatccc cactgaccct ccacacgggtg caaaaatggc tcttggcagc 350  
 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450  
 cactatgtgg gaggacctac ggaaacccat gttgtaaggt ccccatatcc 500  
 ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550  
 tgcaccgttt tcccccaaca tcctccctga ggcaacgtcc tgagccgcag 600  
 gtgacagggga ctgtaggcct gcatctgggg gtaacccct ctgtgatccg 650  
 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700  
 acagccaagc ctgtgcccag ttcttgagc agtatttcca tgactcagac 750  
 ctggctcagt tcctgcgcct ctccggtggc aactttgcac atcaggcatc 800  
 agtagcccggt gtggttgagc aacagggccg gggccgggcc gggattgagg 850  
 ccagtctaga tgtgcagtac ctgatgagtg ctggtgccaa catctccacc 900  
 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttccctgca 950  
 gtgggtcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000  
 tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050  
 gtcaacactg agctcatgaa ggctgccgct cggggtctca ccctgctctt 1100  
 cgctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
 agttccgccc taccttcctt gcctccagcc cctatgtcac cacagtggga 1200  
 ggcacatcct tccaggaacc ttctctcatc acaaataaaa ttgttgacta 1250  
 tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
 aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350  
 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtgggtca gcaacagagt gccattcca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg ccgccccctt cttggctttc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtccctg tctggatgaa gaggtagagg gccagggttt ctgctctgg 1650  
 cctggctggg atcctgtaac aggtggggga acaccaactt cccagctttg 1700  
 ctgaagactc tactcaaccc ctgacctttt cctatcagga gagatggctt 1750  
 gtccccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgg 1800  
 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aaccctgaaa tgctgtgagc ttgacttgac tcccaacctt accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcaactattt 2050  
 acttgatatt cattccccaa ttcactgcaa ggagacctct actgtcaccc 2100  
 tttactcttt cctacctga catccagaaa caatggcctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10					15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

Asn Ile Ser Thr	Trp Val Tyr Ser Ser	Pro Gly Arg His Glu Gly	
	290	295	300
Gln Glu Pro Phe	Leu Gln Trp Leu Met	Leu Leu Ser Asn Glu Ser	
	305	310	315
Ala Leu Pro His	Val His Thr Val Ser	Tyr Gly Asp Asp Glu Asp	
	320	325	330
Ser Leu Ser Ser	Ala Tyr Ile Gln Arg	Val Asn Thr Glu Leu Met	
	335	340	345
Lys Ala Ala Ala	Arg Gly Leu Thr Leu	Leu Phe Ala Ser Gly Asp	
	350	355	360
Ser Gly Ala Gly	Cys Trp Ser Val Ser	Gly Arg His Gln Phe Arg	
	365	370	375
Pro Thr Phe Pro	Ala Ser Ser Pro Tyr	Val Thr Thr Val Gly Gly	
	380	385	390
Thr Ser Phe Gln	Glu Pro Phe Leu Ile	Thr Asn Glu Ile Val Asp	
	395	400	405
Tyr Ile Ser Gly	Gly Gly Phe Ser Asn	Val Phe Pro Arg Pro Ser	
	410	415	420
Tyr Gln Glu Glu	Ala Val Thr Lys Phe	Leu Ser Ser Ser Pro His	
	425	430	435
Leu Pro Pro Ser	Ser Tyr Phe Asn Ala	Ser Gly Arg Ala Tyr Pro	
	440	445	450
Asp Val Ala Ala	Leu Ser Asp Gly Tyr	Trp Val Val Ser Asn Arg	
	455	460	465
Val Pro Ile Pro	Trp Val Ser Gly Thr	Ser Ala Ser Thr Pro Val	
	470	475	480
Phe Gly Gly Ile	Leu Ser Leu Ile Asn	Glu His Arg Ile Leu Ser	
	485	490	495
Gly Arg Pro Pro	Leu Gly Phe Leu Asn	Pro Arg Leu Tyr Gln Gln	
	500	505	510
His Gly Ala Gly	Leu Phe Asp Val Thr	Arg Gly Cys His Glu Ser	
	515	520	525
Cys Leu Asp Glu	Glu Val Glu Gly Gln	Gly Phe Cys Ser Gly Pro	
	530	535	540
Gly Trp Asp Pro	Val Thr Gly Trp Gly	Thr Pro Thr Ser Gln Leu	
	545	550	555

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

```

gccgcgcgct ctctcccggc gccacacct gtctgagcgg cgcagcgcgc 50
cgcgccccgg gcgggctgct cggcgcgga cagtgcctcg catggcaggg 100
attccagggc tctcttctct tctcttcttt ctgctctgtg ctggtgggca 150
agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200
tccctgtcgt cttgccccag tctacctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgc cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actacccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcttaaagc ccaagttaa agatggtggt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900
gcagctgcc a gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggggt 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

```

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaatacg cccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggcttca tgttcttatt ttaggagagg 1300  
 ccaaattggt tttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactgggtt tactatttga aaactgggtt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcag agaaataaaa aaaatactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5				10						15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
				20					25					30
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
				35					40					45
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50					55					60
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65					70					75
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
				80					85					90
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95					100					105
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110					115					120



Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtggg ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct cctgctgct gctggcgtcg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca ccaactgcgc gggtctctgc tcaccagccg 300  
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctgggtgct ctcgagcgt 500  
 ccatacagtt ctcagagcgg gtccctgccca tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac ccaactgctg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
 ttctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
 gccgagcgca acaggccccg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc cccgcctgta 1100  
 aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 267  
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
ggggaattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 269  
gaatgccctg caagcatcaa ctgg 24

<210> 270  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggtc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcagggtc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcacgcatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggcy actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



agatgaggag aaacgtttga tggtaggagct gcacaacctc taccggggccc 150  
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggggccacaa 250  
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
 tacaacctca gcgcggccac ctgcagccca ggccagatgt gcggccacta 400  
 cacgcagggtg gtatggggcca agacagagag gatcggctgt ggttcccact 450  
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650  
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
 aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
 cagaggtctc aggtccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
 caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850  
 ggctccacct tgcgtaacaa ctgagggtccc ttccattttg gcagctcaca 900  
 gctgcccctc cttggatgag gagccagtta cttcccccaa atcgacccat 950  
 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000  
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050  
 caagggaact cctaccccat gccaggagg aggctgaggc tgaggctgag 1100  
 ttgcctcctt ccagtgaggt cttggcctca gtttttccag ccaggacaa 1150  
 gccagggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
 agtccttgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
 gggcgtgccc tggtctgca gtcgtccttg ccagggtgag agggccctga 1300  
 caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350  
 gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

ttctgaatgg gataccactc aaaggggtgaa gaggtcagct gtccctcctgt 1450  
 catcttcccc accctgtccc cagccccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcaggac gaggggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
1				5					10					15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
			20						25					30
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
			35						40					45
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
			50						55					60
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
			65						70					75
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
			80						85					90
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
			95						100					105
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
			110						115					120
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
			125						130					135

Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu
				140					145					150
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr
				155					160					165
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly
				170					175					180
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser
				185					190					195
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro
				200					205					210
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser
				215					220					225
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile
				230					235					240
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys
				245					250					255
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr
				260					265					270
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr
				275					280					285
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu
				290					295					300
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile
				305					310					315
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser
				320					325					330
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly
				335					340					345
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu
				350					355					360
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro
				365					370					375
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr
				380					385					390
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser
				395					400					405

Ala Thr Ala Asn	Ala Thr Gly Gly Arg	Ala Leu Ala Leu Gln Ser
410	415	420
Ser Leu Pro Gly	Ala Glu Gly Pro Asp Lys	Pro Ser Val Val Ser
425	430	435
Gly Leu Asn Ser	Gly Pro Gly His Val Trp	Gly Pro Leu Leu Gly
440	445	450
Leu Leu Leu Leu	Pro Pro Leu Val Leu	Ala Gly Ile Phe
455	460	

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

tcattctcca agttatgggtg gacgtacttc tgttgttctc cctctgcttg 100  
ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
attacacttc tctccttggc tggaaacagg attggtgaaa tactccctga 300  
acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350  
atatttcaga gctccaaact gcatttccag cctacagct caaatatctg 400  
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttg 600  
tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700  
aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750  
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
ttatcaagggt tagatgattc aagcttcctt ggccctaagct tactaaatac 900  
actgcacatt ggggaacaaca gagtcagcta cattgctgat tgtgccttcc 950  
gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000  
tggactattg aagacatgaa tgggtgcttc tctgggcttg acaaactgag 1050  
gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100  
tcactgggtt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150  
atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
gcatttaaata acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250  
cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300  
gccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg	tgtgatgatt	ttcccaaacc	ccagatcacg	gttcagccag	1400
aaacacagtc	ggcaataaaa	ggttccaatt	tgagtttcat	ctgctcagct	1450
gccagcagca	gtgattcccc	aatgactttt	gcttggaaaa	aagacaatga	1500
actactgcat	gatgctgaaa	tggaaaatta	tgcacacctc	cgggcccagg	1550
gtggcgaggt	gatggagtat	accaccatcc	ttcggctgcg	cgaggtggaa	1600
tttgccagtg	aggggaaata	tcagtgtgtc	atctccaatc	actttggttc	1650
atcctactct	gtcaaagcca	agcttacagt	aaatatgctt	ccctcattca	1700
ccaagacccc	catggatctc	accatccgag	ctggggccat	ggcacgcttg	1750
gagtgtgctg	ctgtggggca	cccagcccc	cagatagcct	ggcagaagga	1800
tgggggcaca	gacttcccag	ctgcacggga	gagacgcatg	catgtgatgc	1850
ccgaggatga	cgtgttcttt	atcgtggatg	tgaagataga	ggacattggg	1900
gtatacagct	gcacagctca	gaacagtgc	ggaagtattt	cagcaaattg	1950
aactctgact	gtcctagaaa	caccatcatt	tttgcgcca	ctgttggaac	2000
gaactgtaac	caaggagaaa	acagccgtcc	tacagtgc	tgctggagga	2050
agccctcccc	ctaaactgaa	ctggaccaa	gatgatagcc	cattggtggt	2100
aaccgagagg	cacttttttg	cagcaggcaa	tcagcttctg	attattgtgg	2150
actcagatgt	cagtgatgct	gggaaataca	catgtgagat	gtctaacacc	2200
cttggcactg	agagaggaaa	cgtgcgcctc	agtgtgatcc	ccactccaac	2250
ctgcgaactcc	cctcagatga	cagccccatc	gttagacgat	gacggatggg	2300
ccactgtggg	tgtcgtgatc	atagccgtgg	tttgctgtgt	ggtgggcacg	2350
tcactcgtgt	gggtgggtcat	catataccac	acaaggcgga	ggaatgaaga	2400
ttgcagcatt	accaacacag	atgagaccaa	cttgccagca	gatattccta	2450
gttattttgtc	atctcaggga	acgttagctg	acaggcagga	tgggtacgtg	2500
tcttcagaaa	gtggaagcca	ccaccagttt	gtcacatctt	caggtgctgg	2550
atttttctta	ccacaacatg	acagtagtgg	gacctgccat	attgacaata	2600
gcagtgaagc	tgatgtggaa	gtgtccacag	atctgttctt	ttgtccgttt	2650
ttgggatcca	caggccctat	gtatttgaag	ggaaatgtgt	atggctcaga	2700

tccttttgaa acatatcata caggttgagc tcctgaccca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800  
 tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950  
 agtgcaaatc cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaatc acatttgtac ctttaaacag actttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagaccaa ggaagagctt aacatactac ctcaagttaa cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaaacta 3450  
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500  
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaataaa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10					15

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25					30

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			



				290					295					300
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile
				305					310					315
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg
				320					325					330
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala
				335					340					345
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn
				350					355					360
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys
				365					370					375
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys
				380					385					390
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln
				395					400					405
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly
				410					415					420
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp
				425					430					435
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala
				440					445					450
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser
				455					460					465
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
				470					475					480
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln
				485					490					495
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu
				500					505					510
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn
				515					520					525
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn
				530					535					540
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg
				545					550					555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser	815	820	825
Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr	830	835	840
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr	845	850	855
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr	860	865	870
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His	875	880	885
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr	890	895	900
Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His	905	910	915
Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp	920	925	930
Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn	935	940	945
Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu	950	955	960
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn	965	970	975
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu	980	985	990
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg	995	1000	1005
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly	1010	1015	1020
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn	1025	1030	1035
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro	1040	1045	1050
Asn Phe Gln Ser Tyr Asp Leu Asp Thr	1055		

<210> 291  
 <211> 2906

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

```

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50
ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100
tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
ttggtgtggt ctgacataaa taaataatct taaagcagct gttccctccc 300
ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatatttttg gaatgaaaag tttggggcct ttttagtaaa gttaaagaact 450
ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
tttgtgcta tgttgactaa aattgacgga taattgcagt tggatttttc 650
ttcatcaacc tccttttttt taaattttta ttctttttgg tatcaagatc 700
atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750
gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggtccta ggtttaacag ggccctattt gacccctgc ttgtggtgct 900
gctggtctct caacttcttg tgggtggtgg tctggtgcgg gctcagacct 950
gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000
cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100
agcacttgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150
accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200
actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

```

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100101102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200201202203204205206207208209210211212213214215216217218219220221222223224225226227228229230231232233234235236237238239240241242243244245246247248249250251252253254255256257258259260261262263264265266267268269270271272273274275276277278279280281282283284285286287288289290291292293294295296297298299300301302303304305306307308309310311312313314315316317318319320321322323324325326327328329330331332333334335336337338339340341342343344345346347348349350351352353354355356357358359360361362363364365366367368369370371372373374375376377378379380381382383384385386387388389390391392393394395396397398399400401402403404405406407408409410411412413414415416417418419420421422423424425426427428429430431432433434435436437438439440441442443444445446447448449450451452453454455456457458459460461462463464465466467468469470471472473474475476477478479480481482483484485486487488489490491492493494495496497498499500501502503504505506507508509510511512513514515516517518519520521522523524525526527528529530531532533534535536537538539540541542543544545546547548549550551552553554555556557558559560561562563564565566567568569570571572573574575576577578579580581582583584585586587588589590591592593594595596597598599600601602603604605606607608609610611612613614615616617618619620621622623624625626627628629630631632633634635636637638639640641642643644645646647648649650651652653654655656657658659660661662663664665666667668669670671672673674675676677678679680681682683684685686687688689690691692693694695696697698699700701702703704705706707708709710711712713714715716717718719720721722723724725726727728729730731732733734735736737738739740741742743744745746747748749750751752753754755756757758759760761762763764765766767768769770771772773774775776777778779780781782783784785786787788789790791792793794795796797798799800801802803804805806807808809810811812813814815816817818819820821822823824825826827828829830831832833834835836837838839840841842843844845846847848849850851852853854855856857858859860861862863864865866867868869870871872873874875876877878879880881882883884885886887888889890891892893894895896897898899900901902903904905906907908909910911912913914915916917918919920921922923924925926927928929930931932933934935936937938939940941942943944945946947948949950951952953954955956957958959960961962963964965966967968969970971972973974975976977978979980981982983984985986987988989990991992993994995996997998999100010011002100310041005100610071008100910101011101210131014101510161017101810191020102110221023102410251026102710281029103010311032103310341035103610371038103910401041104210431044104510461047104810491050105110521053105410551056105710581059106010611062106310641065106610671068106910701071107210731074107510761077107810791080108110821083108410851086108710881089109010911092109310941095109610971098109911001101110211031104110511061107110811091110111111121113111411151116111711181119112011211122112311241125112611271128112911301131113211331134113511361137113811391140114111421143114411451146114711481149115011511152115311541155115611571158115911601161116211631164116511661167116811691170117111721173117411751176117711781179118011811182118311841185118611871188118911901191119211931194119511961197119811991200120112021203120412051206120712081209121012111212121312141215121612171218121912201221122212231224122512261227122812291230123112321233123412351236123712381239124012411242124312441245124612471248124912501251125212531254125512561257125812591260126112621263126412651266126712681269127012711272127312741275127612771278127912801281128212831284128512861287128812891290129112921293129412951296129712981299130013011302130313041305130613071308130913101311131213131314131513161317131813191320132113221323132413251326132713281329133013311332133313341335133613371338133913401341134213431344134513461347134813491350135113521353135413551356135713581359136013611362136313641365136613671368136913701371137213731374137513761377137813791380138113821383138413851386138713881389139013911392139313941395139613971398139914001401140214031404140514061407140814091410141114121413141414151416141714181419142014211422142314241425142614271428142914301431143214331434143514361437143814391440144114421443144414451446144714481449145014511452145314541455145614571458145914601461146214631464146514661467146814691470147114721473147414751476147714781479148014811482148314841485148614871488148914901491149214931494149514961497149814991500150115021503150415051506150715081509151015111512151315141515151615171518151915201521152215231524152515261527152815291530153115321533153415351536153715381539154015411542154315441545154615471548154915501551155215531554155515561557155815591560156115621563156415651566156715681569157015711572157315741575157615771578157915801581158215831584158515861587158815891590159115921593159415951596159715981599160016011602160316041605160616071608160916101611161216131614161516161617161816191620162116221623162416251626162716281629163016311632163316341635163616371638163916401641164216431644164516461647164816491650165116521653165416551656165716581659166016611662166316641665166616671668166916701671167216731674167516761677167816791680168116821683168416851686168716881689169016911692169316941695169616971698169917001701170217031704170517061707170817091710171117121713171417151716171717181719172017211722172317241725172617271728172917301731173217331734173517361737173817391740174117421743174417451746174717481749175017511752175317541755175617571758175917601761176217631764176517661767176817691770177117721773177417751776177717781779178017811782178317841785178617871788178917901791179217931794179517961797179817991800180118021803180418051806180718081809181018111812181318141815181618171818181918201821182218231824182518261827182818291830183118321833183418351836183718381839184018411842184318441845184618471848184918501851185218531854185518561857185818591860186118621863186418651866186718681869187018711872187318741875187618771878187918801881188218831884188518861887188818891890189118921893189418951896189718981899190019011902190319041905190619071908190919101911191219131914191519161917191819191920192119221923192419251926192719281929193019311932193319341935193619371938193919401941194219431944194519461947194819491950195119521953195419551956195719581959196019611962196319641965196619671968196919701971197219731974197519761977197819791980198119821983198419851986198719881989199019911992199319941995199619971998199920002001200220032004200520062007200820092010201120122013201420152016201720182019202020212022202320242025202620272028202920302031203220332034203520362037203820392040204120422043204420452046204720482049205020512052205320542055205620572058205920602061206220632064206520662067206820692070207120722073207420752076207720782079208020812082208320842085208620872088208920902091209220932094209520962097209820992100210121022103210421052106210721082109211021112112211321142115211621172118211921202121212221232124212521262127212821292130213121322133213421352136213721382139214021412142214321442145214621472148214921502151215221532154215521562157215821592160216121622163216421652166216721682169217021712172217321742175217621772178217921802181218221832184218521862187218821892190219121922193219421952196219721982199220022012202220322042205220622072208220922102211221222132214221522162217221822192220222122222223222422252226222722282229223022312232223322342235223622372238223922402241224222432244224522462247224822492250225122522253225422552256225722582259226022612262226322642265226622672268226922702271227222732274227522762277227822792280228122822283228422852286228722882289229022912292229322942295229622972298229923002301230223032304230523062307230823092310231123122313231423152316231723182319232023212322232323242325232623272328232923302331233223332334233523362337233823392340234123422343234423452346234723482349235023512352235323542355235623572358235923602361236223632364236523662367236823692370237123722373237423752376237723782379238023812382238323842385238623872388238923902391239223932394239523962397239823992400240124022403240424052406240724082409241024112412241324142415241624172418241924202421242224232424242524262427242824292430243124322433243424352436243724382439244024412442244324442445244624472448244924502451245224532454245524562457245824592460246124622463246424652466246724682469247024712472247324742475247624772478247924802481248224832484248524862487248824892490249124922493249424952496249724982499250025012502250325042505250625072508250925102511251225132514251525162517251825192520252125222523252425252526252725282529253025312532253325342535253625372538253925402541254225432544254525462547254825492550255125522553255425552556255725582559256025612562256325642565256625672568256925702571257225732574257525762577257825792580258125822583258425852586258725882589259025912592259325942595259625972598259926002601260226032604260526062607260826092610261126122613261426152616261726182619262026212622262326242625262626272628262926302631263226332634263526362637263826392640264126422643264426452646264726482649265026512652265326542655265626572658265926602661266226632664266526662667266826692670267126722673267426752676267726782679268026812682268326842685268626872688268926902691269226932694269526962697269826992700270127022703270427052706270727082709271027112712271327142715271627172718271927202721272227232724272527262727272827292730273127322733273427352736273727382739274027412742274327442745274627472748274927502751275227532754275527562757275827592760276127622763276427652766276727682769277027712772277327742775277627772778277927802781278227832784278527862787278827892790279127922793279427952796279727982799280028012802280328042805280628072808280928102811281228132814281528162817281828192820282128222823282428252826282728282829283028312832283328342835283628372838283928402841284228432844284528462847284828492850285128522853285428552856285728582859286028612862286328642865286628672868286928702871287228732874287528762877287828792880288128822883288428852886288728882889289028912892289328942895289628972898289929002901290229032904290529062907290829092910291129122913291429152916291729182919292029212922292329242925292629272928292929302931293229332934293529362937293829392940294129422943294429452946294729482949295029512952295329542955295629572958295929602961296229632964296529662967296829692970297129722973297429752976297729782979298029812982298329842985298629872988298929902991299229932994299529962997299829993000300130023003300430053006300730083009301030113012301330143015301630173018301930203021302230233024302530263027302830293030303130323033303430353036303730383039304030413042304330443045304630473048304930503051305230533054305530563057305830593060306130623063306430653066306730683069307030713072307330743075307630773078307930803081308230833084308530863087308830893090309130923093309430953096309730983099310031013102310331043105310631073108310931103111311231133114311531163117311831193120312131223123312431253126312731283129

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300  
 ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350  
 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggctctgt 1400  
 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450  
 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
 tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550  
 aactgtggat gatacagtc cagattcaag tgattgaacg gaatgccttt 1600  
 gacaaccttc agtcactagt ggagatcaac ctggcacaca ataactaac 1650  
 attactgcct catgacctct tcaactccctt gcatcatcta gagcggatac 1700  
 atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750  
 tgggtggataa aagacatggc cccctcgaac acagcttggt gtgcccggtg 1800  
 taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850  
 attacttcac atgctatgct ccggtgattg tggagcccc tgcagacctc 1900  
 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950  
 cctgacatct gtatcttga ttactccaaa tggaaacagtc atgacacatg 2000  
 gggcgtacaa agtgccgata gctgtgctca gtgatggtac gttaaatttc 2050  
 acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100  
 ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150  
 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200  
 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccaactcc 2250  
 agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300  
 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350  
 agtgggatcc caggaattga tgaggctatg aagactacca aaatcatcat 2400  
 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450  
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500  
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550

catggaaagc cacctgcccc tgccctgctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcacatgaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750  
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850  
 aaaagaaaag aaatattttt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu	Arg Arg Leu Asp Leu Gly	
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser	Glu Gly Ala Phe Glu Gly	
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu	Ala Met Cys Asn Leu Arg	
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile	Lys Leu Asp Glu Leu Asp	
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile	Arg Pro Gly Ser Phe Gln	
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp	Met Ile Gln Ser Gln Ile	
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp	Asn Leu Gln Ser Leu Val	
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu	Thr Leu Leu Pro His Asp	
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu	Arg Ile His Leu His His	
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile	Leu Trp Leu Ser Trp Trp	
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr	Ala Cys Cys Ala Arg Cys	
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg	Tyr Ile Gly Glu Leu Asp	
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro	Val Ile Val Glu Pro Pro	
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met	Ala Ala Glu Leu Lys Cys	
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val	Ser Trp Ile Thr Pro Asn	
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr	Lys Val Arg Ile Ala Val	
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr	Asn Val Thr Val Gln Asp	
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50



gtttccctcc tgcgtgtttgg gggcatgaaa gggcttcgcc gccgggagta 100  
aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
gcgcgggctg ggagcttcgg gtagagacct aggcgcgtgg accgcgatga 250  
gcgcgccgag cctccgtgcg cgcgccgcgg ggttggggct gctgctgtgc 300  
gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350  
cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400  
gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450  
cccagaccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500  
attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550  
aagtgaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600  
gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700  
ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750  
ctcaaatatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
gtattttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850  
accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900  
catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000  
cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050  
cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100  
cttgctgatg ctgcaggaac ttcatctcag ccaaaatgcc atcaacagga 1150  
tcagccctga tgccctgggag ttctgccaga agctcagtga gctggaccta 1200  
actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250  
cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300  
attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

aatgaaat ttt cctggactat tgaagacatg aatgggtgctt tctctgggct 1400  
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
ctaaaaaagc cttcactggg ttggatgcat tggagcatct agacctgagt 1500  
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
actgcaacaa ttgcatttaa atacatcaag ccttttgtgc gattgccagc 1600  
taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700  
tgttagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
cggttcagcc agaaacacag tcggcaataa aaggttcaa tttgagt ttc 1800  
atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850  
aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900  
tccgggcccc aggtggcgag gtgatggagt ataccaccat ccttcggctg 1950  
cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctccaa 2000  
tcactttggg tcatcctact ctgtcaaagc caagcttaca gtaaatatgc 2050  
ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100  
atggcacgct tggagtgtgc tgctgtgggg caccagccc cccagatagc 2150  
ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200  
tgcatgtgat gcccgaggat gacgtgttct ttatcgtgga tgtgaagata 2250  
gaggacattg ggggtatacag ctgcacagct cagaacagtg caggaagtat 2300  
ttcagcaaat gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350  
cactgttgga ccgaactgta accaaggag aaacagccgt cctacagtgc 2400  
attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450  
cccattgggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600  
ccccactcca acctgcgact cccctcagat gacagcccca tcgttagacg 2650  
atgacggatg ggccactgtg ggtgtcgtga tcatagccgt gggttgctgt 2700

gtggtgggca cgtcactcgt gtgggtgggc atcatatacc acacaaggcg 2750  
 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800  
 cagatattcc tagttatttg tcatctcagg gaacgttage tgacaggcag 2850  
 gatgggtacg tgtcttcaga aagtggaagc caccaccagt ttgtcacatc 2900  
 ttcagggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950  
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100  
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
 gagtgetacc catgtttctca tccttcagaa gaatcctgcg aacggagctt 3200  
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300  
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350  
 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400  
 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450  
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500  
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550  
 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600  
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650  
 aacttttatt taaaagagag agaatcttat gttttttaaa tggagttatg 3700  
 aattttaaaa ggataaaaat gctttattta tacagatgaa ccaaaattac 3750  
 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800  
 ctttttaaac tattttttta ctttgtttta tgcaaaaaag tatcttacgt 3850  
 aaattaatga tataaatcat gattatttta tgtattttta taatgccaga 3900  
 tttcttttta tggaaaatga gttactaaag catttttaaat aataacctgcc 3950  
 ttgtaccatt ttttaaatag aagttacttc attatatattt gcacattata 4000

tttaataaaaa tgtgtcaatt tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met	Ser	Ala	Pro	Ser	Leu	Arg	Ala	Arg	Ala	Ala	Gly	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly	20	25	30	
Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg	35	40	45	
Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys	50	55	60	
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp	65	70	75	
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys	80	85	90	
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	95	100	105	
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	110	115	120	
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	125	130	135	
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	140	145	150	
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	155	160	165	
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	170	175	180	
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	185	190	195	
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	200	205	210	
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn				

				215						220					225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	
				230					235					240	
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	
				245					250					255	
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	
				260					265					270	
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	
				275					280					285	
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	
				290					295					300	
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	
				305					310					315	
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	
				320					325					330	
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	
				335					340					345	
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	
				350					355					360	
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	
				365					370					375	
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	
				380					385					390	
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	
				395					400					405	
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	
				410					415					420	
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	
				425					430					435	
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	
				440					445					450	
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	
				455					460					465	
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	
				470					475					480	

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln	740	745	750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	770	775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	785	790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu			

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe



<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

ggggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

cccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gtcc 24

<210> 307

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 308

actccaagga aatcggatcc gttc 24

<210> 309

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcaactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

caaaacttgc gtcgcggaga gcgcccagct tgacttgaat ggaaggagcc 50

cgagcccgcg gagcgcagct gagactgggg gagegcgttc ggctgtggg 100

gcgccgctcg gcgccggggc gcagcaggga aggggaagct gtggtctgcc 150

ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

ccgtccccta tccctccttt atatagaaac cttccacact ggggaaggcag 250

cggcgaggca ggagggtca tggtagcaa ggaggccggc tgatctgcag 300

gcgcacagca ttccgagttt acagatTTTT acagatacca aatggaaggc 350

gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcg 400

atctgactcg gcaccccctg caggcaccat ggcccagagc cgggtgctgc 450  
 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500  
 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550  
 agagaacgaa tttgctggagg aggagccggg gctggtactg agccctgagg 600  
 agcccggggc tggcccagcc gcggtcagct gcccgcgaga ctgtgcctgt 650  
 tcccaggagg gcgtcgtgga ctgtggcggg attgacctgc gtgagttccc 700  
 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccagc 750  
 tggaaaagat ctaccctgag gagctctccc ggctgcaccg gctggagaca 800  
 ctgaacctgc aaaacaaccg cctgacttcc cgaggggtcc cagagaaggc 850  
 gtttgagcat ctgaccaacc tcaattacct gtacttgccc aataacaagc 900  
 tgaccttggc acccgccttc ctgccaaacg ccctgatcag tgtggacttt 950  
 gctgccaaact atctcaccaa gatctatggg ctacaccttg gccagaagcc 1000  
 aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050  
 tgccgggacaa catgttcaac ggctccagca acgtcgaggc cctcatcctg 1100  
 tccagcaact tcctgcgcca cgtgcccag cacctgccgc ctgccctgta 1150  
 caagctgcac ctcaagaaca acaagctgga gaagatcccc ccggggggcct 1200  
 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250  
 actgacgagg gcctggacaa cgagaccttc tggaagctct ccagcctgga 1300  
 gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350  
 cgcgcagcct ggtgctgctg cacttgagga agaacgccat ccggagcgtg 1400  
 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450  
 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500  
 tcaagcgggt gcacacggtg cacctgtaca acaacgcgct ggagcgcgtg 1550  
 cccagtggcc tgcctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600  
 gatcacaggc attggccgcg aagactttgc caccacctac ttctggagg 1650  
 agctcaacct cagctacaac cgcataacca gcccacaggt gcaccgcgac 1700

gccttccgca agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750  
 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800  
 tcaagcgcaa tgagctggct gccttggcac gaggggctcg ggcgggcatg 1850  
 gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900  
 cctgggcccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950  
 tcgccgggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000  
 gagtaacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050  
 cttcgactcc acgccc aacc tcaaggggat ctttctcagg tttaacaagc 2100  
 tggctgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150  
 caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200  
 ccgtggccgc ttgggggaagg aaaaggagga ggaggaagag gaggaggagg 2250  
 aggaagagga aacaagatag tgacaagggtg atgcagatgt gacctaggat 2300  
 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350  
 cccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400  
 tcccacatga cacgggctga cacagtctca tatccccacc cttccccacg 2450  
 gcgtgtccca cggccagaca catgcacaca catcacacc tcaaacaccc 2500  
 agctcagcca cacacaacta cctccaaac caccacagtc tctgtcacac 2550  
 cccactacc gctgccacgc cctctgaatc atgcaggga gggctctgcc 2600  
 ctgccctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650  
 tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcgaa 2700  
 cagccctcca aagcctatgc cacagacagc tcttgcccca gccagaatca 2750  
 gccatagcag ctgcgctct gccctgtcca tctgtccgtc cgttccctgg 2800  
 agaagacaca agggatatcca tgctctgtgg ccaggtgcct gccaccctct 2850  
 ggaactcaca aaagctggct ttatttcctt tcccatccta tggggacagg 2900  
 agccttcagg actgctggcc tggcctggcc caccctgctc ctccagggtc 2950  
 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000  
 caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100  
 ctgggctgag ccagggagga aggacccagc tgcacctagg agacaccttt 3150  
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatocctat ccctgcaaaa aaaaaa 3296

<210> 311  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 311  
 gcattggccg cgagactttg cc 22

<210> 312  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 312  
 gcggccacgg tccttgga aa tg 22

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 313  
 tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314  
 <211> 3003  
 <212> DNA  
 <213> Homo Sapien

<400> 314  
 gggagggggc tccggggcgc gcgcagcaga cctgctccgg ccgcgcgcct 50  
 cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100



gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450  
 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500  
 gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550  
 gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600  
 acactccagg tgtttgtgag aaaacacggt gccacaggag cagccctgtg 1650  
 gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700  
 gggtgacat caagagcgaa tcacaaagat gattaaaggg ttggaaaaaa 1750  
 agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800  
 agaagactga ggggcaaacc attgatgggt ttcaagtata tgaagggttg 1850  
 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900  
 caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950  
 ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000  
 ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggg 2050  
 taaagatggt cttacccaag gaaaagtaac aaattataga atttcccaa 2100  
 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150  
 taatttggac aaggcttaat ttaggcattt ccctcttgac ctccaatgg 2200  
 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250  
 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300  
 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350  
 cctagtgtgg cggtggtttt caatgtttct tcatggtaaa ggtataagcc 2400  
 tttcatttgt tcaatggatg atgtttcaga tttttttttt ttttaagagat 2450  
 ctttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500  
 cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550  
 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600  
 tcaattggac tctcccagg tccacagaac agtaatat tttgaacaat 2650  
 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700  
 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750



gtagatccat ttttaatggg tcatttcctt tatgggcata taactgcaca 2800  
 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850  
 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
 catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
 tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
 aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu  
 1 5 10 15

Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val  
 20 25 30

Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys  
 35 40 45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys  
 50 55 60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys  
 65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu  
 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met  
 95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met  
 110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met  
 125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg  
 140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg  
 155 160 165

Thr Cys Val Asp	Val Asp Glu Cys Ala	Thr Gly Arg Ala Ser Cys
170	175	180
Pro Arg Phe Arg	Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys
185	190	195
Lys Cys His Lys	Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr
200	205	210
Gln Cys His Asp	Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys
215	220	225
Ser Ser Phe Ala	Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys
230	235	240
Lys Cys Lys Glu	Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr
245	250	255
Ile Pro Lys Val	Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro
260	265	270
Lys Gly Asn Gly	Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn
275	280	285
Trp Ile Pro Asp	Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro
290	295	300
Tyr Ile Pro Pro	Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr
305	310	315
Thr Arg Pro Thr	Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro
320	325	330
Pro Pro Pro Leu	Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr
335	340	345
Thr Pro Glu Arg	Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala
350	355	360
Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365	370	375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val
380	385	390
His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu
395	400	405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
410	415	420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly	Arg Leu Met His Ser Gly	
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys	Val Thr Gly Leu His Ser	
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys	His Gly Ala His Gly Ala	
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His	Gly Trp Arg Gln Thr Gln	
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys	Ser Glu Ser Gln Arg	
500	505	

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggacccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

<213> Homo Sapien

<400> 319

```

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50

tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100

caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150

catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250

caatgcccac atacttactg ggctctgtga ataagtctgt ggttcctgac 300

ttggaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350

tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400

acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450

gttgatgatc ctgtcacaaa gccagtgggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550

gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600

agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650

agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700

tcagtgaaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750

tatggacttc aagtgaattc tgataaaggg ctaaaagtag ggggaagtgtt 800

tactgttgac cttggagagg ccatcctatt tgattgttct gctgattctc 850

atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900

atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagccca 950

gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000

aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050

cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100

atcactattt ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150

atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200

gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

```

ctctcggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300  
 ggattccaag caggtctggt ccagcctctg attgtgtatc ggggcaagat 1350  
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctgg 1500  
 aatcagttaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcagggtt ttcagcatat 1600  
 acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650  
 ggagagtcgt tctcatgctg acgggggagaa cgaaagtac aggggtttcc 1700  
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750  
 acactttcac tatcatcaac actgagacta tctgtctca cctacaaatg 1800  
 tggaaacttt acattgttcg atttttcagc agactttggt ttattaaatt 1850  
 tttattagt ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttatttgtac acaaagtaa taaggatggg tgtcacaaaa 1950  
 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100  
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15
Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30
Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45
His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu			

320										325					330				
Ala	Gln	Lys	Gly	Lys	Ser	Leu	Ser	Pro	Leu	Ala	Ser	Ile	Thr	Gly					
335										340					345				
Ile	Ser	Leu	Phe	Leu	Ile	Ile	Ser	Met	Cys	Leu	Leu	Phe	Leu	Trp					
350										355					360				
Lys	Lys	Tyr	Gln	Pro	Tyr	Lys	Val	Ile	Lys	Gln	Lys	Leu	Glu	Gly					
365										370					375				
Arg	Pro	Glu	Thr	Glu	Tyr	Arg	Lys	Ala	Gln	Thr	Phe	Ser	Gly	His					
380										385					390				
Glu	Asp	Ala	Leu	Asp	Asp	Phe	Gly	Ile	Tyr	Glu	Phe	Val	Ala	Phe					
395										400					405				
Pro	Asp	Val	Ser	Gly	Val	Ser	Arg	Ile	Pro	Ser	Arg	Ser	Val	Pro					
410										415					420				
Ala	Ser	Asp	Cys	Val	Ser	Gly	Gln	Asp	Leu	His	Ser	Thr	Val	Tyr					
425										430					435				
Glu	Val	Ile	Gln	His	Ile	Pro	Ala	Gln	Gln	Gln	Asp	His	Pro	Glu					
440										445					450				

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatcctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50  
cctgggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
tggatgatag aattttatgc cccgtgggtgc cctgcttgctc aaaatcttca 200  
accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttata 300  
ataactgctc ttctactat ttatcattgt aaagatgggtg aatttaggcg 350  
ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400  
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650  
accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950  
ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000





aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val  
1 5 10 15

Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn  
20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly  
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400.

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 215 |     | 220 |     | 225 |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Ser | Ala | Gln | Pro | Leu | Lys | Lys | Val | Glu | Glu | Glu | Gln | Glu |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Asp | Glu | Glu | Asp | Val | Ser | Glu | Glu | Glu | Ala | Glu | Ser | Lys | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Gly | Thr | Asn | Lys | Asp | Phe | Pro | Gln | Asn | Ala | Ile | Arg | Gln | Arg | Ser |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |
| Leu | Gly | Pro | Ser | Leu | Ala | Thr | Asp | Lys | Ser |     |     |     |     |     |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgtoct gcaggactca gctgcagggt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgcaaagc cctgatgaga cttcaggaca catacaggct 600

ggaccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700

gaaggggact attatcatatc ggtgttgttg atggagcagg tgctaaagca 750

|            |             |            |            |            |      |
|------------|-------------|------------|------------|------------|------|
| gcttgatgcc | ggggaggagg  | ccaccacaac | caagtcacag | gtgctggact | 800  |
| acctcagcta | tgctgtcttc  | cagttgggtg | atctgcaccg | tgccctggag | 850  |
| ctcaccgcgc | gcctgtcttc  | ccttgaccca | agccacgaac | gagctggagg | 900  |
| gaatctgcgg | tactttgagc  | agttattgga | ggaagagaga | gaaaaaacgt | 950  |
| taacaaatca | gacagaagct  | gagctagcaa | ccccagaagg | catctatgag | 1000 |
| aggcctgtgg | actacctgcc  | tgagagggat | gtttacgaga | gcctctgtcg | 1050 |
| tggggagggg | gtcaaactga  | caccccgtag | acagaagagg | cttttctgta | 1100 |
| ggtaccacca | tggcaacagg  | gccccacagc | tgetcattgc | ccccttcaaa | 1150 |
| gaggaggacg | agtgggacag  | cccgcacatc | gtcaggtact | acgatgtcat | 1200 |
| gtctgatgag | gaaatcgaga  | ggatcaagga | gatcgcaaaa | cctaaacttg | 1250 |
| cacgagccac | cgttcgtgat  | ccaagacag  | gagtcctcac | tgtcgccagc | 1300 |
| taccgggttt | ccaaagctc   | ctggctagag | gaagatgatg | accctgttgt | 1350 |
| ggcccagta  | aatcgtcgga  | tgacgcatat | cacagggtta | acagtaaaga | 1400 |
| ctgcagaatt | gttacagggt  | gcaaattatg | gagtgggagg | acagtatgaa | 1450 |
| ccgcacttcg | acttctctag  | gcgacctttt | gacagcggcc | tcaaaacaga | 1500 |
| ggggaatagg | ttagcgacgt  | ttcttaacta | catgagtgat | gtagaagctg | 1550 |
| gtggtgccac | cgtcttccct  | gatctggggg | ctgcaatttg | gcctaagaag | 1600 |
| ggtacagctg | tgttctggta  | caacctcttg | cggagcgggg | aaggtgacta | 1650 |
| ccgaacaaga | catgctgcct  | gcctgtgtct | tgtgggctgc | aagtgggtct | 1700 |
| ccaataagtg | gttccatgaa  | cgaggacagg | agttcttgag | accttgtgga | 1750 |
| tcaacagaag | ttgactgaca  | tccttttctg | tccttcccct | tcctggtcct | 1800 |
| tcagcccatg | tcaacgtgac  | agacaccttt | gtatgttcct | ttgtatgttc | 1850 |
| ctatcaggct | gattttttgga | gaaatgaatg | tttgtctgga | gcagagggag | 1900 |
| accatactag | ggcgactcct  | gtgtgactga | agtcccagcc | cttccattca | 1950 |
| gcctgtgcca | tccttgggcc  | caaggctagg | atcaaagtgg | ctgcagcaga | 2000 |
| gttagctgtc | tagcgcttag  | caaggctgct | ttgtacctca | ggtgttttag | 2050 |
| gtgtgagatg | tttcagtga   | ccaaagttct | gataccttgt | ttacatgttt | 2100 |

gtttttatgg catttttatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Trp | Val | Ser | Ala | Leu | Leu | Met | Ala | Trp | Phe | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Cys | Val | Gln | Ala | Glu | Phe | Phe | Thr | Ser | Ile | Gly | His | Met |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Leu | Ile | Tyr | Ala | Glu | Lys | Glu | Leu | Val | Gln | Ser | Leu | Lys |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Tyr | Ile | Leu | Val | Glu | Glu | Ala | Lys | Leu | Ser | Lys | Ile | Lys | Ser |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Asn | Lys | Met | Glu | Ala | Leu | Thr | Ser | Lys | Ser | Ala | Ala | Asp |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Gly | Tyr | Leu | Ala | His | Pro | Val | Asn | Ala | Tyr | Lys | Leu | Val |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Leu | Asn | Thr | Asp | Trp | Pro | Ala | Leu | Glu | Asp | Leu | Val | Leu |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asp | Ser | Ala | Ala | Gly | Phe | Ile | Ala | Asn | Leu | Ser | Val | Gln | Arg |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Phe | Phe | Pro | Thr | Asp | Glu | Asp | Glu | Ile | Gly | Ala | Ala | Lys | Ala |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Met | Arg | Leu | Gln | Asp | Thr | Tyr | Arg | Leu | Asp | Pro | Gly | Thr | Ile |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Gly | Glu | Leu | Pro | Gly | Thr | Lys | Tyr | Gln | Ala | Met | Leu | Ser |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Asp | Cys | Phe | Gly | Met | Gly | Arg | Ser | Ala | Tyr | Asn | Glu | Gly |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Tyr | His | Thr | Val | Leu | Trp | Met | Glu | Gln | Val | Leu | Lys | Gln |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Ala | Gly | Glu | Glu | Ala | Thr | Thr | Thr | Lys | Ser | Gln | Val | Leu |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |

|   |     |     |     |
|---|-----|-----|-----|
| Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg | 215 | 220 | 225 |
| Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His | 230 | 235 | 240 |
| Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu | 245 | 250 | 255 |
| Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu | 260 | 265 | 270 |
| Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro | 275 | 280 | 285 |
| Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys | 290 | 295 | 300 |
| Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His | 305 | 310 | 315 |
| Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu | 320 | 325 | 330 |
| Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met | 335 | 340 | 345 |
| Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys | 350 | 355 | 360 |
| Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr | 365 | 370 | 375 |
| Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp | 380 | 385 | 390 |
| Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile | 395 | 400 | 405 |
| Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn | 410 | 415 | 420 |
| Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg | 425 | 430 | 435 |
| Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala | 440 | 445 | 450 |
| Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr | 455 | 460 | 465 |
| Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr | 470 | 475 | 480 |

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe



<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

gcagtattga gttttacttc ctctcttttt tagtggaaga cagaccataa 50  
tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gaccccaggt tctctggtta aaactgaaag 250  
cctactactg gcctggtgcc catcaatcca ttgatccttg aggetgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gcttccccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600  
ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttcctc ggttactcta cttcaactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtgggtg ctcatgggga tgagcggccc 800





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|-----|--|--|--|--|
| 95  |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 100 |  |  |  |  | 105 |  |  |  |  |
| Val | Leu | Thr | Ser | Arg | Ala | Thr | Leu | Ser | Thr | Leu | Ala | Val | Ala | Val |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |  |  |  |  |     |  |  |  |  |
| Asn | Arg | Thr | Val | Ala | His | His | Phe | Pro | Arg | Leu | Leu | Tyr | Phe | Thr |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |  |  |  |  |     |  |  |  |  |
| Gly | Gln | Arg | Gly | Ala | Arg | Ala | Pro | Ala | Gly | Met | Gln | Val | Val | Ser |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |  |  |  |  |     |  |  |  |  |
| His | Gly | Asp | Glu | Arg | Pro | Ala | Trp | Leu | Met | Ser | Glu | Thr | Leu | Arg |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |  |  |  |  |     |  |  |  |  |
| His | Leu | His | Thr | His | Phe | Gly | Ala | Asp | Tyr | Asp | Trp | Phe | Phe | Ile |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |     |  |  |  |  |     |  |  |  |  |
| Met | Gln | Asp | Asp | Thr | Tyr | Val | Gln | Ala | Pro | Arg | Leu | Ala | Ala | Leu |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |  |  |  |  |     |  |  |  |  |
| Ala | Gly | His | Leu | Ser | Ile | Asn | Gln | Asp | Leu | Tyr | Leu | Gly | Arg | Ala |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |  |  |  |  |     |  |  |  |  |
| Glu | Glu | Phe | Ile | Gly | Ala | Gly | Glu | Gln | Ala | Arg | Tyr | Cys | His | Gly |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |  |  |  |  |     |  |  |  |  |
| Gly | Phe | Gly | Tyr | Leu | Leu | Ser | Arg | Ser | Leu | Leu | Leu | Arg | Leu | Arg |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |  |  |  |     |  |  |  |  |
| Pro | His | Leu | Asp | Gly | Cys | Arg | Gly | Asp | Ile | Leu | Ser | Ala | Arg | Pro |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |     |  |  |  |  |
| Asp | Glu | Trp | Leu | Gly | Arg | Cys | Leu | Ile | Asp | Ser | Leu | Gly | Val | Gly |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |  |  |  |  |     |  |  |  |  |
| Cys | Val | Ser | Gln | His | Gln | Gly | Gln | Gln | Tyr | Arg | Ser | Phe | Glu | Leu |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |  |  |  |  |     |  |  |  |  |
| Ala | Lys | Asn | Arg | Asp | Pro | Glu | Lys | Glu | Gly | Ser | Ser | Ala | Phe | Leu |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |  |  |  |  |     |  |  |  |  |
| Ser | Ala | Phe | Ala | Val | His | Pro | Val | Ser | Glu | Gly | Thr | Leu | Met | Tyr |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |  |  |  |  |     |  |  |  |  |
| Arg | Leu | His | Lys | Arg | Phe | Ser | Ala | Leu | Glu | Leu | Glu | Arg | Ala | Tyr |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |  |  |  |  |     |  |  |  |  |
| Ser | Glu | Ile | Glu | Gln | Leu | Gln | Ala | Gln | Ile | Arg | Asn | Leu | Thr | Val |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |  |  |  |  |     |  |  |  |  |
| Leu | Thr | Pro | Glu | Gly | Glu | Ala | Gly | Leu | Ser | Trp | Pro | Val | Gly | Leu |     |  |  |  |  |     |  |  |  |  |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |     |  |  |  |  |     |  |  |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Ala | Pro | Phe | Thr | Pro | His | Ser | Arg | Phe | Glu | Val | Leu | Gly | Trp |  |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |  |
| Asp | Tyr | Phe | Thr | Glu | Gln | His | Thr | Phe | Ser | Cys | Ala | Asp | Gly | Ala |  |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |  |
| Pro | Lys | Cys | Pro | Leu | Gln | Gly | Ala | Ser | Arg | Ala | Asp | Val | Gly | Asp |  |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |  |
| Ala | Leu | Glu | Thr | Ala | Leu | Glu | Gln | Leu | Asn | Arg | Arg | Tyr | Gln | Pro |  |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |  |
| Arg | Leu | Arg | Phe | Gln | Lys | Gln | Arg | Leu | Leu | Asn | Gly | Tyr | Arg | Arg |  |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |  |
| Phe | Asp | Pro | Ala | Arg | Gly | Met | Glu | Tyr | Thr | Leu | Asp | Leu | Leu | Leu |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |  |
| Glu | Cys | Val | Thr | Gln | Arg | Gly | His | Arg | Arg | Ala | Leu | Ala | Arg | Arg |  |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |  |
| Val | Ser | Leu | Leu | Arg | Pro | Leu | Ser | Arg | Val | Glu | Ile | Leu | Pro | Met |  |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Pro | Tyr | Val | Thr | Glu | Ala | Thr | Arg | Val | Gln | Leu | Val | Leu | Pro | Leu |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |  |
| Leu | Val | Ala | Glu | Ala | Ala | Ala | Ala | Pro | Ala | Phe | Leu | Glu | Ala | Phe |  |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |  |
| Ala | Ala | Asn | Val | Leu | Glu | Pro | Arg | Glu | His | Ala | Leu | Leu | Thr | Leu |  |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |  |
| Leu | Leu | Val | Tyr | Gly | Pro | Arg | Glu | Gly | Gly | Arg | Gly | Ala | Pro | Asp |  |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |  |
| Pro | Phe | Leu | Gly | Val | Lys | Ala | Ala | Ala | Ala | Glu | Leu | Glu | Arg | Arg |  |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |  |
| Tyr | Pro | Gly | Thr | Arg | Leu | Ala | Trp | Leu | Ala | Val | Arg | Ala | Glu | Ala |  |
|     |     |     |     | 560 |     |     |     |     | 565 |     |     |     |     | 570 |  |
| Pro | Ser | Gln | Val | Arg | Leu | Met | Asp | Val | Val | Ser | Lys | Lys | His | Pro |  |
|     |     |     |     | 575 |     |     |     |     | 580 |     |     |     |     | 585 |  |
| Val | Asp | Thr | Leu | Phe | Phe | Leu | Thr | Thr | Val | Trp | Thr | Arg | Pro | Gly |  |
|     |     |     |     | 590 |     |     |     |     | 595 |     |     |     |     | 600 |  |
| Pro | Glu | Val | Leu | Asn | Arg | Cys | Arg | Met | Asn | Ala | Ile | Ser | Gly | Trp |  |
|     |     |     |     | 605 |     |     |     |     | 610 |     |     |     |     | 615 |  |
| Gln | Ala | Phe | Phe | Pro | Val | His | Phe | Gln | Glu | Phe | Asn | Pro | Ala | Leu |  |
|     |     |     |     | 620 |     |     |     |     | 625 |     |     |     |     | 630 |  |

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50  
 tgtccccaag ccgttctaga cgcggaataa atgctttctg aaagcagctc 100  
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450  
 aagcttataca atacgccttt gataagtata gagaccaata caactgggtc 500  
 ttccttgacac gcccactac gtttgctatc attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgctt gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
 gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850  
 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900  
 tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatgggggat accgccttag ggcatttggg catattttca atgatgcatt 1000  
 ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100  
 gtaactacat atccaatata gctgtatggt tctttttctt ttctaatttg 1150  
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200  
 ggggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaaa 1250  
 aagtgtttta agaataataa ttttgcaa ataaactattaa taaatattat 1300  
 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
 tttgctgatt ggtaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
 gcaaatgata tctctagttg tgaatttggt attaaagtaa aacttttagc 1450  
 tgtgtgttcc ctttacttct aatactgatt tatgtttctaa gcctcccaa 1500  
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

&lt;400&gt; 341

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Leu | Ser | Glu | Ser | Ser | Ser | Phe | Leu | Lys | Gly | Val | Met | Leu | Gly | 1   | 5   | 10  | 15 |
| Ser | Ile | Phe | Cys | Ala | Leu | Ile | Thr | Met | Leu | Gly | His | Ile | Arg | Ile | 20  | 25  | 30  |    |
| Gly | His | Gly | Asn | Arg | Met | His | His | His | Glu | His | His | His | Leu | Gln | 35  | 40  | 45  |    |
| Ala | Pro | Asn | Lys | Glu | Asp | Ile | Leu | Lys | Ile | Ser | Glu | Asp | Glu | Arg | 50  | 55  | 60  |    |
| Met | Glu | Leu | Ser | Lys | Ser | Phe | Arg | Val | Tyr | Cys | Ile | Ile | Leu | Val | 65  | 70  | 75  |    |
| Lys | Pro | Lys | Asp | Val | Ser | Leu | Trp | Ala | Ala | Val | Lys | Glu | Thr | Trp | 80  | 85  | 90  |    |
| Thr | Lys | His | Cys | Asp | Lys | Ala | Glu | Phe | Phe | Ser | Ser | Glu | Asn | Val | 95  | 100 | 105 |    |
| Lys | Val | Phe | Glu | Ser | Ile | Asn | Met | Asp | Thr | Asn | Asp | Met | Trp | Leu | 110 | 115 | 120 |    |
| Met | Met | Arg | Lys | Ala | Tyr | Lys | Tyr | Ala | Phe | Asp | Lys | Tyr | Arg | Asp | 125 | 130 | 135 |    |
| Gln | Tyr | Asn | Trp | Phe | Phe | Leu | Ala | Arg | Pro | Thr | Thr | Phe | Ala | Ile | 140 | 145 | 150 |    |
| Ile | Glu | Asn | Leu | Lys | Tyr | Phe | Leu | Leu | Lys | Lys | Asp | Pro | Ser | Gln | 155 | 160 | 165 |    |
| Pro | Phe | Tyr | Leu | Gly | His | Thr | Ile | Lys | Ser | Gly | Asp | Leu | Glu | Tyr | 170 | 175 | 180 |    |
| Val | Gly | Met | Glu | Gly | Gly | Ile | Val | Leu | Ser | Val | Glu | Ser | Met | Lys | 185 | 190 | 195 |    |
| Arg | Leu | Asn | Ser | Leu | Leu | Asn | Ile | Pro | Glu | Lys | Cys | Pro | Glu | Gln | 200 | 205 | 210 |    |
| Gly | Gly | Met | Ile | Trp | Lys | Ile | Ser | Glu | Asp | Lys | Gln | Leu | Ala | Val | 215 | 220 | 225 |    |
| Cys | Leu | Lys | Tyr | Ala | Gly | Val | Phe | Ala | Glu | Asn | Ala | Glu | Asp | Ala | 230 | 235 | 240 |    |
| Asp | Gly | Lys | Asp | Val | Phe | Asn | Thr | Lys | Ser | Val | Gly | Leu | Ser | Ile | 245 | 250 | 255 |    |
| Lys | Glu | Ala | Met | Thr | Tyr | His | Pro | Asn | Gln | Val | Val | Glu | Gly | Cys |     |     |     |    |



|                 |                         |                     |     |  |     |
|-----------------|-------------------------|---------------------|-----|--|-----|
|                 | 260                     |                     | 265 |  | 270 |
| Cys Ser Asp Met | Ala Val Thr Phe Asn Gly | Leu Thr Pro Asn Gln |     |  |     |
|                 | 275                     |                     | 280 |  | 285 |
| Met His Val Met | Met Tyr Gly Val Tyr Arg | Leu Arg Ala Phe Gly |     |  |     |
|                 | 290                     |                     | 295 |  | 300 |
| His Ile Phe Asn | Asp Ala Leu Val Phe Leu | Pro Pro Asn Gly Ser |     |  |     |
|                 | 305                     |                     | 310 |  | 315 |

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctgggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc ttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatacgcactcact ataggggtca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 350

ggattctaatacgcactcactatagggcggcgatgtccactggggctac48

<210> 351

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 351

ctatgaaattaacccctcactaaagggacgaggaagatgggcggatgggt48

<210> 352

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 352

ggattctaatacgcactcactatagggcaccacgcgtccggctgctt47

<210> 353

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 353

ctatgaaattaacccctcactaaagggacggggacaccacggaccaga48

<210> 354

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 354

ggattctaatacgcactcactatagggcttgctgcggttttggttcctg48

<210> 355

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 355

ctatgaaatt aaccctcact aaagggagct gccgatccca ctggtatt 48

<210> 356

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 356

ggattctaatt acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 357

ctatgaaatt aaccctcact aaagggagcc cgggcatggt ctcagtta 48

<210> 358

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaatt acgactcact atagggcggg aagatggcga ggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 360  
 ggattctaatacgcactcactatagggctgtgctttcattctgccagta 48

<210> 361  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 361  
 ctatgaaattaacctcactaaagggaggggtacaattaagggtggat 48

<210> 362  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 362  
 ggattctaatacgcactcactatagggcccgctcgctcctgctcctg 47

<210> 363  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 363  
 ctatgaaattaacctcactaaagggaggaatgccgcgacctcacag 48

<210> 364  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaatac gactcact atagggcccc tctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaagggagtgtgtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggattctaatac gactcact atagggcgca gcatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtgt 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggattctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatacgcactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatacgcactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggatttcta at acgactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50  
 agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
 aaaaaatgaa ttcattctaaa tcattctgaaa cacaatgcac agagagagga 150  
 tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gcctgtttca tcaccagatg tggtgtgaca tttcgcatct 250  
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
 ctctctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
 gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400  
 tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450  
 gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500  
 taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggc 550  
 agtggcaatg ggtggacggc acaccttga caaagtctct gagcttctgg 600  
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
 tcaattatct tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750



ggaaaatctc ttttaagaaca gaaggcacaa ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Asn | Ser | Ser | Lys | Ser | Ser | Glu | Thr | Gln | Cys | Thr | Glu | Arg | Gly | 1   | 5   | 10  | 15 |
| Cys | Phe | Ser | Ser | Gln | Met | Phe | Leu | Trp | Thr | Val | Ala | Gly | Ile | Pro | 20  | 25  | 30  |    |
| Ile | Leu | Phe | Leu | Ser | Ala | Cys | Phe | Ile | Thr | Arg | Cys | Val | Val | Thr | 35  | 40  | 45  |    |
| Phe | Arg | Ile | Phe | Gln | Thr | Cys | Asp | Glu | Lys | Lys | Phe | Gln | Leu | Pro | 50  | 55  | 60  |    |
| Glu | Asn | Phe | Thr | Glu | Leu | Ser | Cys | Tyr | Asn | Tyr | Gly | Ser | Gly | Ser | 65  | 70  | 75  |    |
| Val | Lys | Asn | Cys | Cys | Pro | Leu | Asn | Trp | Glu | Tyr | Phe | Gln | Ser | Ser | 80  | 85  | 90  |    |
| Cys | Tyr | Phe | Phe | Ser | Thr | Asp | Thr | Ile | Ser | Trp | Ala | Leu | Ser | Leu | 95  | 100 | 105 |    |
| Lys | Asn | Cys | Ser | Ala | Met | Gly | Ala | His | Leu | Val | Val | Ile | Asn | Ser | 110 | 115 | 120 |    |
| Gln | Glu | Glu | Gln | Glu | Phe | Leu | Ser | Tyr | Lys | Lys | Pro | Lys | Met | Arg | 125 | 130 | 135 |    |
| Glu | Phe | Phe | Ile | Gly | Leu | Ser | Asp | Gln | Val | Val | Glu | Gly | Gln | Trp | 140 | 145 | 150 |    |
| Gln | Trp | Val | Asp | Gly | Thr | Pro | Leu | Thr | Lys | Ser | Leu | Ser | Phe | Trp | 155 | 160 | 165 |    |
| Asp | Val | Gly | Glu | Pro | Asn | Asn | Ile | Ala | Thr | Leu | Glu | Asp | Cys | Ala | 170 | 175 | 180 |    |

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
 215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgacg acaaccgt 18

<210> 383  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgccct tccccaacca 20

<210> 385  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386

cacaaactcg aactgcttct g 21

<210> 387

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggctttggta gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

cacagagcat ttgtccatca gcagttcag 29

<210> 402

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ggcagagact tccagtcact ga 22

<210> 403

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

gccaaaggtg gtgtagata gg 22

<210> 404

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 404

caggccccct tgatctgtac ccca 24

<210> 405

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 405

gggacgtgct tctacaagaa cag 23

<210> 406  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 406  
caggcttaca atgttatgat cagaca 26  
  
<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 407  
tattcagagt tttccattgg cagtgccagt t 31  
  
<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 408  
tctacatcag cctctctgcg c 21  
  
<210> 409  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 409  
cgatcttctc caccagag cg 23  
  
<210> 410  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 410



gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

ctccctgaat ggcagcctga gca 23

<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taaggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 414

tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgcctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

gggactacaa gccgcgccgc gctgccgctg gcccctcagc aaccctcgac 50  
 atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100  
 cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
 tcaaatccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250  
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
 ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
 cggtgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450  
 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500  
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
 ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600  
 ccagagccaa tcccagattt cgcaattott ctttccactt aaactctgaa 650  
 acaggcactt tgggtttcac tgctgttcac aaggacgact ctgggcagta 700  
 ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750



[illegible]

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
gcctttggat ggatgttgc gtacacagat gctacagact tgtactaaca 3500  
caccgtaatt tggcatttgc ttaacctcat ttataaaagc ttcaaaaaaa 3550  
ccca 3554

<210> 423

<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Leu | Arg | Arg | Pro | Pro | Arg | Leu | Arg | Leu | Cys | Ala | Arg | Leu | 1   | 5   | 10  | 15 |
| Pro | Asp | Phe | Phe | Leu | Leu | Leu | Leu | Phe | Arg | Gly | Cys | Leu | Ile | Gly | 20  | 25  | 30  |    |
| Ala | Val | Asn | Leu | Lys | Ser | Ser | Asn | Arg | Thr | Pro | Val | Val | Gln | Glu | 35  | 40  | 45  |    |
| Phe | Glu | Ser | Val | Glu | Leu | Ser | Cys | Ile | Ile | Thr | Asp | Ser | Gln | Thr | 50  | 55  | 60  |    |
| Ser | Asp | Pro | Arg | Ile | Glu | Trp | Lys | Lys | Ile | Gln | Asp | Glu | Gln | Thr | 65  | 70  | 75  |    |
| Thr | Tyr | Val | Phe | Phe | Asp | Asn | Lys | Ile | Gln | Gly | Asp | Leu | Ala | Gly | 80  | 85  | 90  |    |
| Arg | Ala | Glu | Ile | Leu | Gly | Lys | Thr | Ser | Leu | Lys | Ile | Trp | Asn | Val | 95  | 100 | 105 |    |
| Thr | Arg | Arg | Asp | Ser | Ala | Leu | Tyr | Arg | Cys | Glu | Val | Val | Ala | Arg | 110 | 115 | 120 |    |
| Asn | Asp | Arg | Lys | Glu | Ile | Asp | Glu | Ile | Val | Ile | Glu | Leu | Thr | Val | 125 | 130 | 135 |    |
| Gln | Val | Lys | Pro | Val | Thr | Pro | Val | Cys | Arg | Val | Pro | Lys | Ala | Val | 140 | 145 | 150 |    |
| Pro | Val | Gly | Lys | Met | Ala | Thr | Leu | His | Cys | Gln | Glu | Ser | Glu | Gly | 155 | 160 | 165 |    |
| His | Pro | Arg | Pro | His | Tyr | Ser | Trp | Tyr | Arg | Asn | Asp | Val | Pro | Leu | 170 | 175 | 180 |    |
| Pro | Thr | Asp | Ser | Arg | Ala | Asn | Pro | Arg | Phe | Arg | Asn | Ser | Ser | Phe | 185 | 190 | 195 |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Asn | Ser | Glu | Thr | Gly | Thr | Leu | Val | Phe | Thr | Ala | Val | His |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
| Lys | Asp | Asp | Ser | Gly | Gln | Tyr | Tyr | Cys | Ile | Ala | Ser | Asn | Asp | Ala |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Gly | Ser | Ala | Arg | Cys | Glu | Glu | Gln | Glu | Met | Glu | Val | Tyr | Asp | Leu |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Ile | Gly | Gly | Ile | Ile | Gly | Gly | Val | Leu | Val | Val | Leu | Ala | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Leu | Ala | Leu | Ile | Thr | Leu | Gly | Ile | Cys | Cys | Ala | Tyr | Arg | Arg | Gly |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |
| Tyr | Phe | Ile | Asn | Asn | Lys | Gln | Asp | Gly | Glu | Ser | Tyr | Lys | Asn | Pro |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |
| Gly | Lys | Pro | Asp | Gly | Val | Asn | Tyr | Ile | Arg | Thr | Asp | Glu | Glu | Gly |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |
| Asp | Phe | Arg | His | Lys | Ser | Ser | Phe | Val | Ile |     |     |     |     |     |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     |     |

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000